1: L42342. Mus musculus (clo...[gi:848991] ProbeSet, Related Sequences, Protein, Taxonomy, LinkOut

```
LOCUS       MUSSOCHB                1618 bp    mRNA    linear   ROD 06-JUN-1995
DEFINITION  Mus musculus (clone NaCh bc 1.6 in pBS+) sodium channel mRNA,
            complete cds.
ACCESSION   L42342
VERSION     L42342.1  GI:848991
KEYWORDS    sodium channel.
SOURCE      Mus musculus (strain C3H) (clone: NaCh bc 1.6 in pBS+) cDNA to
            mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1618)
  AUTHORS   Jover,E. and Shah,V.
  TITLE     Mouse sodium channel clone BC in pSB+
  JOURNAL   Unpublished (1995)
FEATURES             Location/Qualifiers
     source          1..1618
                     /organism="Mus musculus"
                     /strain="C3H"
                     /db_xref="taxon:10090"
                     /clone="NaCh bc 1.6 in pBS+"
                     /cell_line="BC3H-1"
                     /cell_type="muscle-like cells from brain tumor"
                     /note="(vector lambda gt11)"
     mRNA            1..>1618
     5'UTR           1..46
     CDS             47..1618
                     /codon_start=1
                     /product="sodium channel"
                     /protein_id="AAA68000.1"
                     /db_xref="GI:848992"
                     /translation="MTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFVFDIVTRQAF
                     DIIIMALICLNMITMMVETDNQSEEKTKVLGRINQFFVAVFTGECVMKMFALRQYYFT
                     NGWNVFDFIVVILSISSLLFSAILSSLESYFSPTLLRVIRLARIGRILRLIRAAKGIR
                     TLLFALMMSLPALFNIGLLLFLVMFIYSIFGMASFANVIDEAGIDDMFNFKTFGNSML
                     CLFQITTSAGWDGLLSPILNTGPPYCDPNRPNSNGSKGNCGSPAVGILFFTTYIIISF
                     LIVVNMYIAVILENFNVATEESTEPLSEDDFDMFYETWEKFDPEATQFIAFSALSDFA
                     DTLSGPLRIPKPNQNILIQMDLPLVPGDKIHCLDILFAFTKNVLGESGELDSLKTNME
                     EKFMATNLSKASYEPIATTLRCKQEDISATIIQKAYRNYMLQRSLMLSNPLHVPRAEE
                     DGVSLPREGYVTFMANDNGGLPDKSETASATSFPPSYDSVTRGLSDRANISTSSSMQN
                     EDEVTAKEGKSPGPQ"
BASE COUNT      393 a    466 c    374 g    385 t
ORIGIN
        1 acatcagcag gtccttctcc tctacctagg gggccaggac atcttcatga cagaggagca
       61 gaagaagtac tacaatgcca tgaagaagct gggctccaag aaaccccaga agcccatccc
      121 acggcctttg aataagtacc agggcttcgt gtttgacatt gtgaccaggc aagcatttga
      181 catcatcatc atggctctca tctgcctcaa catgatcacc atgatggtgg agaccgacaa
      241 tcagagcgag gagaagacga aggtcctggg cagaatcaac cagttcttcg tggccgtctt
      301 cacgggcgag tgtgtgatga agatgttcgc ccttcggcag tattacttca ccaacggctg
      361 gaatgtgttc gacttcattg tggtgattct gtccatttct agtctgttgt tttctgcgat
      421 ccttagctca ctagaaagtt acttctcccc cacgctctta cgcgtcatcc gtctggccag
```

```
      481 gatcggccgc atcctcaggc tgattcgagc agccaagggg attcgcacgc tgctcttcgc
      541 cctcatgatg tccctgcccg ccctcttcaa catcggcctc ctcctcttcc tcgtcatgtt
      601 catctactcc atcttcggca tggccagctt cgctaatgtc atagatgagg ctggcatcga
      661 cgacatgttc aacttcaaga cctttggcaa cagcatgctg tgccttttcc agatcaccac
      721 gtcggctggc tgggatggcc tcctcagccc catcctcaac acaggacccc cctactgcga
      781 ccccaaccgg cctaacagca atggctccaa ggggaattgt ggaagcccag cggtgggcat
      841 cctcttcttc accacctaca tcatcatctc cttcctcatc gtggtcaaca tgtacattgc
      901 agtgattctg gagaacttca atgtggccac agaagagagc acggagcccc tgagcgagga
      961 cgactttgac atgttctatg agacctggga gaagtttgac ccggaggcca cccagttcat
     1021 tgccttttct gccctctcag actttgcaga cacactctct ggccctctta gaatcccaaa
     1081 acctaatcag aatatattaa tccagatgga cctgccgttg gtccccggag ataagatcca
     1141 ctgtttggac atcctctttg ccttcacaaa gaatgtcttg ggagaatctg gggagttgga
     1201 ttctctgaag actaatatgg aagagaagtt tatggcaact aatctttcca aagcatccta
     1261 tgaaccaata gcaaccaccc tccggtgcaa gcaggaagac atctcagcca ccattattca
     1321 aaaggcctat cggaactaca tgttgcaacg ctccttgatg ctctccaacc ccctgcatgt
     1381 gcccagggct gaggaggatg gcgtgtcact ccccagggaa ggctatgtta cattcatggc
     1441 aaatgacaac ggtgggctcc cagacaaatc ggaaactgct tctgctacgt ctttcccacc
     1501 atcctatgac agcgtcacca ggggcctgag tgacagggcc aacattagca catctagctc
     1561 aatgcaaaat gaagatgaag tcactgctaa ggaagggaag agccctggac ctcagtga
//
```

Revised: October 24, 2001.

1: M81758. Homo sapiens skel...[gi:338212]

Related Sequences, OMIM, Protein, PubMed, Taxonomy, UniSTS, LinkOut

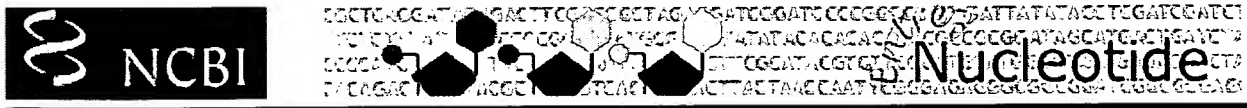
```
LOCUS       HUMSKM1A                7823 bp    mRNA    linear   PRI 13-JAN-1995
DEFINITION  Homo sapiens skeletal muscle voltage-dependent sodium channel alpha
            subunits (SkM1) mRNA, complete cds.
ACCESSION   M81758
VERSION     M81758.1  GI:338212
KEYWORDS    transmembrane protein; voltage-dependent sodium channel alpha
            subunit.
SOURCE      Homo sapiens adult skeletal muscle cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 7823)
  AUTHORS   George,A.L. Jr., Komisarof,J., Kallen,R.G. and Barchi,R.L.
  TITLE     Primary structure of the adult human skeletal muscle
            voltage-dependent sodium channel
  JOURNAL   Ann. Neurol. 31 (2), 131-137 (1992)
  MEDLINE   92246457
   PUBMED   1315496
FEATURES             Location/Qualifiers
     source          1..7823
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="17q23.1-2"
                     /tissue_type="skeletal muscle"
                     /dev_stage="adult"
     gene            1..7823
                     /gene="SkM1"
     5'UTR           1..77
                     /gene="SkM1"
     CDS             78..5588
                     /gene="SkM1"
                     /note="tetrodoxin-sensitive isoform; wild-type sequence of
                     the hyperkalemic periodic paralysis gene;
                     voltage-dependent"
                     /codon_start=1
                     /product="sodium channel alpha subunit"
                     /protein_id="AAA60554.1"
                     /db_xref="GI:338213"
                     /translation="MARPSLCTLARLGPECLRPFTRESLAAIEQRAVEEEARLQRNKQ
                     MEIEEPERKPRSDLEAGKNLPMIYGDPPPEVIGIPLEDLDPYYSNKKTFIVLNKGKAI
                     FRFSATPALYLLSPFSVVRRGAIKVLIHALFSMFIMITILTNCVFMTMSDPPPWSKNV
                     EYTFTGIYTFESLIKILARGFCVDDFTFLRDPWNWLDFSVIMMAYLTEFVDLGNISAL
                     RTFRVLRALKTITVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALVGLQLFMGNL
                     RQKCVRWPPPFNDTNTTWYSNDTWYGNDTWYGNEMWYGNDSWYANDTWNSHASWATND
                     TFDWDAYISDEGNFYFLEGSNDALLCGNSSDAGHCPKGYECIKTGRNPNYGYTSYDTF
                     SWAFLALFRLMTQDYWENLFQLTLRAAGKTYMIFFVVIIFLGSFYLINLILAVVAMAY
                     AEQNEATLAEDKEKEEEFQQMLEKFKKHQEELEKAKAAQALEGGEADGDPAHGKDCNG
                     SLDTSQGEKGAPRQSGSGDSGISDAMEELEEAHQKCPPWWYKCAHKVLIWDCCAPWLK
                     FKNIIHLIVMDPFVDLGITICIVLNTLFMAMEHYPMTEHFDNVLTVGNLVFTGIFTAE
                     MVLKLIAMDPYEYFQQGWNIFDSIIVTLSLVELGLANVQGLSVLRSFRLLRVFKLAKS
```

```
                     WPTLNMLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCKIALDCNLP
                     RWHMHDFFHSFLIVFRILCGEWIETMWDCMEVAGQAMCLTVFLMVMVIGNLVVLNLFL
                     ALLLSSFSADSLAASDEDGEMNNLQIAIGRIKLGIGFAKAFLLGLLHGKILSPKDIML
                     SLGEADGAGEAGEAGETAPEDEKKEPPEEDLKKDNHILNHMGLADGPPSSLELDHLNF
                     INNPYLTIQVPIASEESDLEMPTEEETDTFSEPEDSKKPPQPLYDGNSSVCSTADYKP
                     PEEDPEEQAEENPEGEQPEECFTEACVQRWPCLYVDISQGRGKKWWTLRRACFKIVEH
                     NWFETFIVFMILLSSGALAFEDIYIEQRRVIRTILEYADKVFTYIFIMEMLLKWVAYG
                     FKVYFTNAWCWLDFLIVDVSIISLVANWLGYSELGPIKSLRTLRALRPLRALSRFEGM
                     RVVVNALLGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYYCINTTTSERFDISEVN
                     NKSECESLMHTGQVRWLNVKVNYDNVGLGYLSLLQVATFKGWMDIMYAAVDSREKEEQ
                     PQYEVNLYMYLYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKLGGKDIFMTEEQKKYY
                     NAMKKLGSKKPQKPIPRPQNKIQGMVYDLVTKQAFDITIMILICLNMVTMMVETDDQS
                     QLKVDILYNINMIFIIIFTGECVLKMLALRQYYFTVGWNIFDFVVVILSIVGLALSDL
                     IQKYFVSPTLFRVIRLARIGRVLRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMF
                     IYSIFGMSNFAYVKKESGIDDMFNFETFGNSIICLFEITTSAGWDGLLNPILNSGPPD
                     CDPNLENPGTSVKGDCGNPSIGICFFCSYIIISFLIVVNMYIAIILENFNVATEESSE
                     PLGEDDFEMFYETWEKFDPDATQFIAYSRLSDFVDTLQEPLRIAKPNKIKLITLDLPM
                     VPGDKIHCLDILFALTKEVLGDSGEMDALKQTMEEKFMAANPSKVSYEPITTTLKRKH
                     EEVCAIKIQRAYRRHLLQRSMKQASYMYRHSHDGSGDDAPEKEGLLANTMSKMYGHEN
                     GNSSSPSPEEKGEAGDAGPTMGLMPISPSDTAWPPAPPPGQTVRPGVKESLV"
     3'UTR           5589..7823
                     /gene="SkM1"
BASE COUNT     1621 a   2354 c   2147 g   1701 t
ORIGIN      Chromosome 17q23.1-25.3.
        1 ccagcacccc ggggctgcgc actgcagctc cccaggccac ccaccaccct tctggtctct
       61 gagcccagga tgcgaggatg gccagaccat ctctgtgcac cctggctcgt ctgggccctg
      121 agtgcttgcg ccccttcacc cgggagtcac tggcagccat agaacagcgg gcggtggagg
      181 aggaggcccg gctgcagcgg aataagcaga tggagattga ggagcccgaa cggaagccac
      241 gaagtgactt ggaggctggc aagaacctac ccatgatcta cggagacccc ccgccggagg
      301 tcatcggcat ccccctggag gacctggatc cctactacag caataagaag accttcatcg
      361 tactcaacaa gggcaaggcc atcttccgct tctccgccac acctgctctc tacctgctga
      421 gcccccttcag cgtagtcagg cgcggggcca tcaaggtgct catccatgcg ctgttcagca
      481 tgttcatcat gatcaccatc ttgaccaact gcgtattcat gaccatgagt gacccgcctc
      541 cctggtccaa gaatgtggag tacaccttca cagggatcta caccttgag tccctcatca
      601 agatactggc ccgaggcttc tgtgtcgacg acttcacatt cctccgggac ccctggaact
      661 ggctggactt cagtgtcatc atgatggcgt acctgacaga gtttgtggac ttgggcaaca
      721 tctcagccct gaggaccttc cgggtgctgc gggccctcaa aaccatcacg gtcatcccag
      781 ggctgaagac gatcgtgggg gccctgatcc agtcggtgaa gaagctgtcg gatgtgatga
      841 tcctcactgt cttctgcctg agcgtctttg cgctggtagg actgcagctc ttcatgggaa
      901 acctgaggca gaagtgtgtg cgctggcccc cgccgttcaa cgacaccaac accacgtggt
      961 acagcaatga cacgtggtac ggcaatgaca catggtatgg caatgagatg tggtacggca
     1021 atgactcatg gtatgccaac gacacgtgga acagccatgc aagctgggcc accaacgata
     1081 cctttgattg ggacgcctac atcagtgatg aagggaactt ctacttcctg gagggctcca
     1141 acgatgccct gctctgtggg aacagcagtg atgctgggca ctgccctaag ggttatgagt
     1201 gcatcaagac cgggcggaac cccaactatg gctacaccag ctatgacacc ttcagctggg
     1261 ccttcttggc tctcttccgc ctcatgacac aggactattg ggagaacctc ttccagctga
     1321 cccttcgagc agctggcaag acctacatga tcttcttcgt ggtcatcatc ttcctgggct
     1381 ctttctacct catcaatctg atcctggccg tggtggccat ggcatatgcc gagcagaatg
     1441 aggccaccct ggccgaggat aaggagaaag aggaggagtt tcagcagatg cttgagaagt
     1501 tcaaaaagca ccaggaggag ctggagaagg ccaaggccgc ccaagctctg gaaggtgggg
     1561 aggcagatgg ggacccagcc catggcaaag actgcaatgg cagcctggac acatcgcaag
     1621 gggagaaggg agccccgagg cagagcggca gcggagacag cggcatctcc gacgccatgg
     1681 aagaactgga agaggcccac caaaagtgcc caccatggtg gtacaagtgc gcccacaaag
     1741 tgctcatatg ggactgctgc gccccgtggc tgaagttcaa gaacatcatc cacctgatcg
     1801 tcatggaccc gttcgtggac ctgggcatca ccatctgcat cgtgctcaac accctcttca
     1861 tggccatgga acattacccc atgacggagc actttgacaa cgtgctcact gtgggcaacc
     1921 tggtcttcac aggcatcttc acagcagaga tggttctgaa gctgattgcc atggacccct
     1981 acgagtattt ccagcagggt tggaatatct tcgacagcat catcgtcacc ctcagcctgg
     2041 tagagctagg cctggccaac gtacagggac tgtctgtgct acgctccttc cgtctgctgc
     2101 gggtcttcaa gctggccaag tcgtggccaa cgctgaacat gctcatcaag atcattggca
     2161 attcagtggg ggcgctgggt aacctgacgc tggtgctggc tatcatcgtg ttcatcttcg
     2221 ccgtggtggg catgcagctg tttggcaaga gctacaagga gtgcgtgtgc aagattgcct
     2281 tggactgcaa cctgccgcgc tggcacatgc atgatttctt ccactccttc ctcatcgtct
     2341 tccgcatcct gtgcggggag tggatcgaga ccatgtggga ctgcatggag gtggccggcc
     2401 aagccatgtg cctcaccgtc ttcctcatgg tcatggtcat cggcaatctt gtggtcctga
```

```
2461 acctgttcct ggctctgctg ctgagctcct tcagcgccga cagtctggca gcctcggatg
2521 aggatggcga gatgaacaac ctgcagattg ccatcgggcg catcaagttg ggcatcggct
2581 ttgccaaggc cttcctcctg gggctgctgc atggcaagat cctgagcccc aaggacatca
2641 tgctcagcct cggggaggct gacggggccg gggaggctgg agaggcgggg gagactgccc
2701 ccgaggatga gaagaaggag ccgcccgagg aggacctgaa gaaggacaat cacatcctga
2761 accacatggg cctggctgac ggccccccat ccagcctcga gctggaccac cttaacttca
2821 tcaacaaccc ctacctgacc atacaggtgc ccatcgcctc cgaggagtcc gacctggaga
2881 tgcccaccga ggaggaaacc gacactttct cagagcctga ggatagcaag aagccgccgc
2941 agcctctcta tgatgggaac tcgtccgtct gcagcacagc tgactacaag ccccccgagg
3001 aggaccctga ggagcaggca gaggagaacc ccgaggggga gcagcctgag gagtgcttca
3061 ctgaggcctg cgtgcagcgc tggccctgcc tctacgtgga catctcccag ggccgtggga
3121 agaagtggtg gactctgcgc agggcctgct tcaagattgt cgagcacaac tggttcgaga
3181 ccttcattgt cttcatgatc ctgctcagca gtggggctct ggccttcgag gacatctaca
3241 ttgagcagcg gcgagtcatt cgcaccatcc tagaatatgc cgacaaggtc ttcacctaca
3301 tcttcatcat ggagatgctg ctcaaatggg tggcctacgg ctttaaggtg tacttcacca
3361 acgcctggtg ctggctcgac ttcctcatcg tggatgtctc catcatcagc ttggtggcca
3421 actggctggg ctactcggag ctgggaccca tcaaatccct gcggacactg cgggccctgc
3481 gtcccctgag ggcactgtcc cgattcgagg gcatgagggt ggtggtgaac gccctcctag
3541 gcgccatccc ctccatcatg aatgtgctgc ttgtctgcct catcttctgg ctgatcttca
3601 gcatcatggg tgtcaacctg tttgccggca agttctacta ctgcatcaac accaccacct
3661 ctgagaggtt cgacatctcc gaggtcaaca acaagtctga gtgcgagagc ctcatgcaca
3721 caggccaggt ccgctggctc aatgtcaagg tcaactacga caacgtgggt ctgggctacc
3781 tctccctcct gcaggtggcc accttcaagg gttggatgga catcatgtat gcagccgtgg
3841 actcccggga gaaggaggag cagccgcagt acgaggtgaa cctctacatg tacctctact
3901 ttgtcatctt catcatcttt ggctccttct tcaccctcaa cctcttcatt ggcgtcatca
3961 ttgacaactt caaccagcag aagaagaagt taggggggaa agacatcttt atgacggagg
4021 aacagaagaa atactataac gccatgaaga agcttggctc caagaagcct cagaagccaa
4081 ttccccggcc ccagaacaag atccagggca tggtgtatga cctcgtgacg aagcaggcct
4141 tcgacatcac catcatgatc ctcatctgcc tcaacatggt caccatgatg gtggagacag
4201 acgaccagag ccagctcaag gtggacatcc tgtacaacat caacatgatc ttcatcatca
4261 tcttcacagg ggagtgcgtg ctcaagatgc tcgccctgcg ccagtactac ttcaccgttg
4321 gctggaacat ctttgacttc gtggtcgtca tcctgtccat tgtgggcctt gccctctctg
4381 acctgatcca gaagtacttc gtgtcaccca cgctgttccg tgtgatccgc ctggcgcgga
4441 ttgggcgtgt cctgcggctg atccgcgggg ccaagggcat ccggacgctg ctgttcgccc
4501 tcatgatgtc gctgcctgcc ctcttcaaca tcggcctcct cctcttcctg gtcatgttca
4561 tctactccat cttcggcatg tccaactttg cctacgtcaa gaaggagtcg ggcatcgatg
4621 atatgttcaa cttcgagacc ttcggcaaca gcatcatctg cctgttcgag atcaccacgt
4681 cggccggctg ggacgggctc ctcaacccca tcctcaacag cgggcccccа gactgtgacc
4741 ccaacctgga gaacccgggc accagtgtca agggtgactg cggcaacccc tccatcggca
4801 tctgcttctt ctgcagctat atcatcatct ccttcctcat cgtggtcaac atgtacatcg
4861 ccatcatcct ggagaacttc aatgtggcca cagaggagag cagcgagccc cttggtgaag
4921 atgactttga gatgttctac gagacatggg agaagttcga ccccgacgcc acccagttca
4981 tcgcctacag ccgcctctca gacttcgtgg acaccctgca ggaaccgctg aggattgcca
5041 agcccaacaa gatcaagctc atcacactgg acttgcccat ggtgccaggg gacaagatcc
5101 actgcctgga catcctcttt gccctgacca aagaggtcct gggtgactct ggggaaatgg
5161 acgccctcaa gcagaccatg gaggagaagt tcatggcagc caacccctcc aaggtgtcct
5221 acgagcccat caccaccacc ctcaagagga agcacgagga ggtgtgcgcc atcaagatcc
5281 agagggccta ccgccggcac ctgctacagc gctccatgaa gcaggcatcc tacatgtacc
5341 gccacagcca cgacggcagc ggggatgacg cccctgagaa ggaggggctg cttgccaaca
5401 ccatgagcaa gatgtatggc cacgagaatg ggaacagcag ctcgccaagc ccggaggaga
5461 agggcgaggc aggggacgcc ggacccacta tggggctgat gcccatcagc ccctcagaca
5521 ctgcctggcc tcccgccccc cccccagggc agactgtgcg cccaggtgtc aaggagtctc
5581 ttgtctagca ggcagcatcg gggtggcccc actgagtctc ggcatagtcc ccagagctcc
5641 cccgtggtgc ctgcacacag agtgagggag gagggctttg aatctgggac tgtgcctggc
5701 tccctgatgg gggacaggat ttggccacac tggggctgac acccaggccc gagcgcctgc
5761 gttcccagac catgggaaat gggaattgcg ctcaggggct ccatgctggg tctgaggccc
5821 ctgcctccaa gatttaacct gcaagttgct ctgacctcct ctgggccctg tcgcccctcc
5881 ttttggcctg ggggaggtca gaacattcga atctctgccc ctcacttgag gaggagctgg
5941 cctgcggtgg agggatcagt tgcccccat caccagagtc ttaagggtca ctggcctctc
6001 cccaggaagt gggctcagac ccccctcagc cccagcccag acaaagatgt cttaacctca
6061 gggagtgcag acacctaacc ccagggcact gccagcccac ccccttttgac tctggggtgc
6121 agcttcaccc accaggccag ctcaggaatt ccctggaaaa gggaaatgtg actggttcag
6181 aaatagctcc tcaaagcctc aaaacctgat tggccactgg atcctgctgc tttgggctgg
6241 gatggtgact cctgaaacct cttcctaggc cacgtccagg tccgtagctc ccctggctgg
6301 ctcctagggg aagagcagaa ggaaggatgc cacttgggaa tgaattgtcc ttttctagga
```

```
     6361 agcacggggg agtgagacag gctgggtcct gccagctgga tcgctgcaca tggcctgagc
     6421 atccagacct gagcgggagt cagggacctg ctgctcagta agaagattct cgccccttcc
     6481 ctctctccct gcctcactcc tccgtgagca ccaccagggc tccaggagcc tcatccagcc
     6541 tcagagatct cccttctcat ctccccacgc cccgtctctt tctcaccttt cccacctctc
     6601 tccccaaagt gatcctaaga atgtacagtt gagctcaggt tagatatttc gaccctgggg
     6661 cgtgcagcag ggaaggccca actggttcag gctcaacctt ccaacttcct gtggcctgaa
     6721 gaagcacttc tgctgcatcg ctgttctggg catggcaggg ccaggcctct gctggctcag
     6781 gaggaggggt gagagacctg ctcaggcgtc gctggattta ttcacttgtg tgtgtacctg
     6841 tggctgtgtg tctgcttgta tgcttttata ggcctgtgtg tatagctgtg tgtgtgttca
     6901 agtgcgtgac tgtatgtgtg tgtgtgaacc actgtgtgaa ccactgtgta ctggagcctg
     6961 cattatgcac gtgtctgggt atctttgtat atatgtgtat atatgtgtgc cctggactgt
     7021 ttcaaggtcc atggagtacg gctggtgtgt catactgtgc aggcctgtcc ctgggagtgt
     7081 tcccgtgcct gggagagtgg acctgtgctg tgagtgtgtg gatgcgtgtg aacgcatgtg
     7141 gtaaggtgtg tactcagggc attctgttgg cctaagtgcc tcttcttttt cttcttgttt
     7201 ctcatgaaaa gtttgattaa aattcaggaa gcagcaaaac cttcaaaaca agacatgtat
     7261 gtgtgcttga gtgtgtgaac acgtgtgtgt gtgtgcacat ctacatgcca tgcctatggg
     7321 ccagagttgt ctttattgtc caccatgctc tctcacctgc ttcccagtcc tgcctgaaca
     7381 gccctctctc tcactccccc ctcctccccc tcctgtttct cgttgtcaca cccatggcct
     7441 cagccctgct ccctgcctcc tgcctatgtc tcctctatgg aaggaggcct ccactccttc
     7501 catctcttcc ttcagaagtt tcgtctaatg ggggcagtct ccccttcctg gcacattgcc
     7561 cctctgcctt gccctcctgg gccctgggct ggcacagccc ctggagcctc agaaatctgt
     7621 ttgattggat attctcctcg gactgtgtgc aggttgcaga ggaagagtag atgagccggg
     7681 tccggcctct ccctgcctgt ggcccctccc ctgcagacgg atgcccattc ctgcctggtc
     7741 cagtggggaa caggtcccac gccaggccag caggcgggct cctttgtaca gttcttacaa
     7801 taaaccctcc ttggtgcctc tgg
//
```

Revised: October 24, 2001.



1: M26643. Rat skeletal musc...[gi:205651]

Related Sequences, Protein, PubMed, Taxonomy, UniSTS, LinkOut

```
LOCUS       RATNCHVS                6957 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Rat skeletal muscle voltage-sensitive sodium channel alpha subunit
            mRNA, complete cds.
ACCESSION   M26643
VERSION     M26643.1  GI:205651
KEYWORDS    ion channel; voltage-sensitive sodium channel.
SOURCE      Rat (strain Wistar) skeletal muscle, cDNA to mRNA, clones
            pRM[1,3,9,10,11].
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 6957)
  AUTHORS   Trimmer,J.S., Cooperman,S.S., Tomiko,S.A., Zhou,J., Crean,S.M.,
            Boyle,M.B., Kallen,R.G., Sheng,Z., Barchi,R.L., Sigworth,F.J.,
            Goodman,R.H., Agnew,W.S. and Mandel,G.
  TITLE     Primary structure and functional expression of a mammalian skeletal
            muscle sodium channel
  JOURNAL   Neuron 3 (1), 33-49 (1989)
  MEDLINE   90148778
   PUBMED   2559760
COMMENT     Draft entry and computer-readable sequence for [1] kindly provided
            by J.S.Trimmer, 02-AUG-1989.
FEATURES             Location/Qualifiers
     source          1..6957
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     CDS             450..5972
                     /note="voltage-sensitive sodium channel alpha subunit"
                     /codon_start=1
                     /protein_id="AAA41682.1"
                     /db_xref="GI:205652"
                     /translation="MASSSLPNLVPPGPHCLRPFTPESLAAIEQRAVEEEARLQRNKQ
                     MEIEEPERKPRSDLEAGKNLPLIYGDPPPEVIGIPLEDLDPYYSDKKTFIVLNKGKAI
                     FRFSATPALYLLSPFSIVRRVAIKVLIHALFSMFIMITILTNCVFMTMSNPPSWSKHV
                     EYTFTGIYTFESLIKMLARGFCIDDFTFLRDPWNWLDFSVITMAYVTEFVDLGNISAL
                     RTFRVLRALKTITVIPGLKTIVGALIQSVKKLSDVMILTVFCLSVFALVGLQLFMGNL
                     RQKCVRWPPPMNDTNTTWYGNDTWYSNDTWYGNDTWYINDTWNSQESWAGNSTFDWEA
                     YINDEGNFYFLEGSNDALLCGNSSDAGHCPEGYECIKAGRNPNYGYTSYDTFSWAFLA
                     LFRLMTQDYWENLFQLTLRAAGKTYMIFFVVIIFLGSFYLINLILAVVAMAYAEQNEA
                     TLAEDQEKEEEFQQMLEKYKKHQEELEKAKAAQALESGEEADGDPTHNKDCNGSLDAS
                     GEKGPPRPSCSADSAISDAMEELEEAHQKCPPWWYKCAHKVLIWNCCAPWVKFKHIIY
                     LIVMDPFVDLGITICIVLNTLFMAMEHYPMTEHFDNVLSVGNLVFTGIFTAEMVLKLI
                     AMDPYEYFQQGWNIFDSFIVTLSLVELGLANVQGLSVLRSFRLLRVFKLAKSWPTLNM
                     LIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCKIASDCNLPRWHMND
                     FFHSFLIVFRILCGEWIETMWDCMEVAGQAMCLTVFLMVMVIGNLVVLNLFLALLLSS
                     FSADSLAASDEDGEMNNLQIAIGRIKWGIGFAKTFLLGLLRGKILSPKEIILSLGEPG
                     GAGENAEESTPEDEKKEPPPEDKELKDNHILNHVGLTDGPRSSIELDHLNFINNPYLT
                     IQVPIASEESDLEMPTEEETDAFSEPEDIKKPLQPLYDGNSSVCSTADYKPPEEDPEE
                     QAEENPEGEQPEECFTEACVKRCPCLYVDISQGRGKMWWTLRRACFKIVEHNWFETFI
```

VFMILLSSGALAFEDIYIEQRRVIRTILEYADKVFTYIFILEMLLKWVAYGFKVYFTN
AWCWLDFLIVDVSIISLVANWLGYSELGPIKSLRTLRALRPLRALSRFEGMRVVVNAL
LGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFYYCVNTTTSERFDISVVNNKSESES
LMYTGQVRWMNVKVNYDNVGLGYLSLLQVATFKGWMDIMYAAVDSREKEEQPHYEVNL
YMYLYFVIFIIFGSFFTLNLFIGVIIDNFNQQKKKFGGKDIFMTEEQKKYYNAMKKLG
SKKPQKPIPRPQNKIQGMVYDFVTKQVFDISIMILICLNMVTMMVETDDQSQLKVDIL
YNINMVFIIIFTGECVLKMFALRHYYFTIGWNIFDFVVVILSIVGLALSDLIQKYFVS
PTLFRVIRLARIGRVLRLIRGAKGIRTLLFALMMSLPALFNIGLLLFLVMFIYSIFGM
SNFAYVKKESGIDDMFNFETFGNSIICLFEITTSAGWDGLLNPILNSGPPDCDPTLEN
PGTNVRGDCGNPSIGICFFCSYIIISFLIVVNMYIAIILENFNVATEESSEPLSEDDF
EMFYETWEKFDPDATQFIDYSRLSDFVDTLQEPLKIAKPNKIKLITLDLPMVPGDKIH
CLDILFALTKEVLGDSGEMDALKQTMEEKFMAANPSKVSYEPITTTLKRKQEEVCAIK
IQRAYRRHLLQRSVKQASYMYRHSQDGNDDGAPEKEGLLANTMNKMYGHEKEGDGVQS
QGEEEKASTEDAGPTVEPEPTSSSDTALTPSPPPLPPSSSPPQGQTVRPGVKESLV"

BASE COUNT 1547 a 2027 c 1850 g 1533 t

ORIGIN

```
       1 acggcacccg gggctcgtcc gccaccgctc ttctctgctt ctggccaaca gctgaagtca
      61 cgcagttcct ggagtctgaa cccaggagac agttcgggac actggggcgt tggccccaag
     121 ctcctcgggc tggagaagat ctggttcact ttctgttgat cccgaaggtg gcacaatcta
     181 ttgctgagaa gagaacactg cggggcctgg agtgggggaa tgcaccgtgc ccagtgtcct
     241 gggcatcagc acgcccaggt cttgcaggca catctcccag ccccaacaag accaggacac
     301 ccacctccct gacccaactc ctgggcaggc agagagtgag gagtacacag tagaccccgg
     361 gcattggtga ccacccaaaa cccaagggct gcgggctgta gcggctctgt tacctaccac
     421 cctctggccc ctgagcccag aatgcaagga tggccagctc atctctgccc aacctggtcc
     481 ccccgggtcc ccactgcctg cgccccttca ccccagagtc cctggcagcc atagagcagc
     541 gggcggtgga ggaggaggcc cggctgcagc ggaacaagca gatggagatt gaggagcctg
     601 agcggaagcc acgcagtgac ctggaagctg gcaagaacct cccactcatc tatggggacc
     661 ccccacccga agtcattggc atccccctgg aggacctgga tccttactac agtgacaaga
     721 agaccttcat tgtgctcaac aaaggaaagg ccatcttccg attctctgcc acgcctgccc
     781 tctacctgct gagccccttc agcatcgtca ggagggtggc tatcaaggtg ctcattcacg
     841 cgctgttcag catgtttatc atgatcacca tcctgaccaa ctgtgtgttc atgaccatga
     901 gcaatccgcc ttcttggtcc aaacacgtgg agtacacctt cacggggatc tatacctttg
     961 agtccctcat taagatgctg gcccgaggct tttgcattga tgacttcaca ttcctccgag
    1021 acccctggaa ctggctggac ttcagtgtca tcacaatggc gtatgtgaca gagtttgtgg
    1081 acttgggcaa catctcagcc ctgaggacct tccgtgtgct gcgggccctg aagaccatca
    1141 cggttatccc agggctgaag acaattgtgg gagccctgat ccagtctgtg aaaaagctgt
    1201 cggatgtgat gatcctcact gtcttctgcc tgagtgtctt tgccctggtg gggctgcagc
    1261 ttttcatggg aaacctgcgt cagaagtgcg tgcgttggcc cccgcccatg aatgacacca
    1321 acaccacgtg gtatggcaat gacacttggt acagcaatga cacttggtac ggcaatgaca
    1381 cttggtacat caatgacact tggaacagcc aggagagctg ggccggcaac tctacctttg
    1441 actgggaggc ctacatcaat gacgaaggga acttctattt cttggagggc tccaatgatg
    1501 ctctgctctg tgggaatagc agtgatgctg ggcactgccc tgagggctac gaatgcataa
    1561 aggctgggcg gaaccccaac tatggctaca ccagctatga caccttcagc tgggctttcc
    1621 tggctctctt ccggctcatg acgcaggact actgggagaa ccttttccag ctgaccctac
    1681 gagctgctgg caagacctac atgatcttct tcgtggtcat catcttcctg ggctccttct
    1741 acctcatcaa tctgatcctg gccgtggtgg ccatggcgta cgctgagcag aatgaggcta
    1801 ccctggccga agaccaggag aaagaggagg agttccaaca gatgcttgag aaatacaaaa
    1861 aacatcagga ggaactggaa aaggctaagg ctgcccaggc tctggaaagt ggagaggagg
    1921 cagatgggga cccaacccac aacaaagact gcaatgggag cctggatgca tccggggaga
    1981 aggggccccc aaggccaagc tgcagcgcag acagtgccat ctcagatgct atggaggagc
    2041 tggaagaggc ccatcagaag tgcccaccgt ggtggtacaa gtgtgcacac aaagtcctca
    2101 tctggaactg ctgtgccccg tgggtgaagt tcaaacatat aatctacctg atcgtcatgg
    2161 acccctttgt ggacctgggt atcaccatct gcattgtgct caacaccctc ttcatggcca
    2221 tggagcacta ccccatgacc gagcactttg acaacgtgct ctccgtgggc aacttggtct
    2281 tcacaggcat cttcactgcg gagatggtgt tgaagctgat tgccatggac ccctacgagt
    2341 atttccaaca gggctggaac atctttgaca gtttcatcgt caccctcagc ctggtggagc
    2401 tgggcctggc caacgtacag gggctgtcag tgctccgttc cttccgcctg ctgcgtgtct
    2461 tcaagctggc caagtcatgg ccaacactca acatgctcat caaaatcatt ggcaactcag
    2521 tgggcgcgct gggcaacctg accctggtgc tggccatcat cgtcttcatc ttcgccgtgg
    2581 tgggcatgca gctgttcggc aagagctata aggagtgtgt gtgcaagatc gcctcagact
    2641 gcaacctgcc tcgctggcac atgaacgact tcttccactc cttcctcatc gtcttccgca
    2701 tcctctgcgg ggaatggatc gagaccatgt gggactgcat ggaggtggcc ggccaggcca
    2761 tgtgcctcac cgtcttcctc atggtcatgg tcattggcaa cctggtggtc ctgaatctgt
    2821 tcctggctct cctgctgagt tccttcagtg ctgacagcct ggcggcctcg gatgaggatg
    2881 gcgagatgaa caacctacag attgccatcg ggcgtatcaa gtggggcatc ggttttgcca
```

```
2941 aaaccttcct cctggggctg ttgcgtggca agatcctgag ccccaaggaa ataatactca
3001 gcctcggtga gcccgggggt gccggggaaa atgccgagga gagtactccc gaggatgaga
3061 agaaggagcc gccaccggaa gataaggagc tgaaagacaa tcatatcctg aaccacgtgg
3121 gcctgaccga tggcccccgc tccagcatcg agctggacca ccttaacttc atcaacaacc
3181 cctacctcac catccaggtg cccattgcct ccgaggagtc tgacctggag atgcccacag
3241 aggaggagac agacgccttc tcggagcctg aggatatcaa gaagccccta cagcccctct
3301 acgacgggaa ctcctccgtc tgcagcacag ctgactacaa gccccctgaa gaggaccccg
3361 aggagcaggc tgaggagaac cccgaggggg agcagcctga ggaatgcttc acggaagcct
3421 gtgtgaagcg ctgcccctgc ctctatgtgg acatctccca gggccgtggg aaaatgtggt
3481 ggacactgcg cagggcctgt ttcaagattg ttgagcacaa ctggtttgag accttcattg
3541 tcttcatgat cttgctcagc agtggagccc tggccttcga ggacatctac attgaacagc
3601 gacgagtcat ccgcaccatc ctggaatacg ccgacaaggt cttcacctac atcttcatcc
3661 tggagatgtt gctaaagtgg gtcgcctacg gcttcaaggt gtatttcacc aatgcctggt
3721 gctggctcga cttcctcatc gtggacgtct ccatcatcag cctggtggca aactggctgg
3781 gctactctga gctggggccc atcaaatccc tgcgcacact ccgggccctg cgacctctga
3841 gggcactgtc tcgatttgag ggtatgaggg tggtggtgaa cgccctcctg ggagctatcc
3901 cctccatcat gaacgtcctc ctcgtctgcc tcatcttctg gctcatcttc agcatcatgg
3961 gggtcaactt gtttgctgga aagttctact actgcgtcaa caccaccacc tctgagagat
4021 tcgacatctc ggtggtcaac aacaagtccg agtctgagag cctcatgtat acaggccagg
4081 tccgctggat gaatgtcaag gtcaactacg acaacgtggg tctgggctat ctctccctcc
4141 ttcaggtggc cacattcaag ggttggatgg atatcatgta tgcagctgtg gactcccggg
4201 agaaagagga gcagccacac tatgaggtga acctctacat gtacctctac ttcgtcatct
4261 tcatcatctt cggctccttc ttcaccctca acctcttcat cggtgtcatc atcgacaact
4321 tcaaccaaca gaagaagaag tttggaggga aagacatctt catgacagag gaacagaaga
4381 aatactacaa tgcgatgaag aagcttggct ccaagaagcc ccagaagcca attccccggc
4441 ctcagaacaa gatccagggc atggtgtacg acttcgtgac gaagcaggtg tttgacatct
4501 ccatcatgat cctcatctgc ctcaacatgg ttactatgat ggtggagaca gatgaccaga
4561 gccagctcaa ggtggacatc ctgtacaaca tcaacatggt cttcattatc atcttcacag
4621 gggagtgtgt gctgaagatg tttgccctac gccattacta cttcaccatt ggctggaaca
4681 tctttgactt tgtggttgtc atcttgtcca tcgtgggcct tgcgctctct gacttgatac
4741 agaaatactt tgtgtcaccc acgctgttcc gtgtgatccg cttggctcgg atcgggcgtg
4801 tcctgcgtct gatccgcggg gccaagggca tccggacgct gctgttcgcc ctgatgatgt
4861 ccctgcccgc cctcttcaac atcggcctcc ttctctttct ggtcatgttc atctactcga
4921 tcttcggcat gtctaacttc gcctacgtca agaaagagtc aggcatcgac gacatgttta
4981 actttgagac ctttggcaac agtatcatct gcctcttcga gatcaccacg tcagccggct
5041 gggacgggct tctgaacccc atcctcaaca gtgggccccc agactgtgac ccgacgttgg
5101 agaacccggg taccaatgtc agggggact gcggcaaccc ttccatcggc atctgtttct
5161 tctgcagcta catcatcatc tccttcctca tcgtggtcaa catgtacatt gctatcatcc
5221 tggagaattt caacgtggcc accgaagaga gcagcgagcc cctcagtgag gatgacttcg
5281 agatgttcta tgagacctgg gagaagttcg acccggacgc cactcagttc atcgactaca
5341 gccgcctctc ggactttgtg gacaccctgc aggagccact gaaaatcgcc aaacccaata
5401 agatcaagct tatcacgtta gacctgccca tggtgcccgg cgacaagatc cactgcttgg
5461 acatcctctt tgccctgacc aaagaggtac tgggtgactc tggggagatg gacgccctca
5521 agcagaccat ggaggagaag tttatggcag ctaacccttc caaggtctcc tatgagccca
5581 tcaccaccac cctcaagagg aagcaggagg aggtgtgtgc tatcaaaatc cagagggcct
5641 accgccgcca cctgctgcag cgctccgtga agcaggcctc ttacatgtac cgtcacagcc
5701 aggacggcaa tgacgacggg gcccccgaga aggagggatt gcttgccaac accatgaaca
5761 agatgtatgg ccatgagaaa gagggtgatg gtgtgcagag ccaggggggag gaagagaagg
5821 cctctacaga ggatgctgga cccaccgtgg agcccgaacc caccagcagc tcagatactg
5881 ccctgactcc ttctcctcca ccactacccc cctcatcatc accgccacaa gggcagacag
5941 ttcgcccagg ggtcaaagag tctcttgtct agatggcagc gtcaaggctg cacgcagagt
6001 tggaggggaa gggctttgag atgggggcta tacaggactt gacacctggg ctgaggggta
6061 tggaaattgt gctcagggtt caggtgggtc ggaagcccct gctgcctgat ttcatcttta
6121 cgatgctctg acattctgtt ggccagggga ggccaggaca tctgaatgct gtttccttct
6181 tgggggagag ccagcatacc ttggaggggt tggccacctt cctgtcacta ctttaagggc
6241 ccaggacccc agctctagcc aagacaaaga cgaatcttaa cccccaaacc tacacctgac
6301 ccccagagct tagctatccc tctcgccccc ataattctag ggtgcagctt ccccctgaca
6361 gctcaggaat gccctgtaaa aggggaaatg gttctggtac agaaccaatt ggccgctgga
6421 tccggatgta tcaggctgga aacatgactt ctgaaacctt tcacccagtc agatccaggc
6481 cggtgggcag ctcccctggc tggcccctgg gggaagaact aaggaaggat tgccctgaga
6541 aattaccttt ctctagattg cgtggatggg tcaaacaggc tgggtcctgc cagctgcatt
6601 catgcccttg agcctgagcg cccacatctg cctggggtca ggttggaagc tctctatcaa
6661 gaatcgcccg ttcccgcctc cctgccttct ttctttgaat accagggctc ctgggagccc
6721 catcaaacac gaaagactgc cttcctcctg tctaatctct gccccccccc tccctgcccc
6781 ttccctgctt cctcaagtga ctctgagaat gctagaactc agcacacggg agatgagttg
```

```
     6841 atactggggc atgcagtgag aaggctcacc aggcttggct ttggtcttct cattgcctga
     6901 aagcaagttt tcccctgaga cagggtttct tttctccgtg tagccctggc tgcctgg
//
```

Revised: October 24, 2001.

1: P15389. SODIUM CHANNEL PR...[gi:116452]

BLink, Related Sequences, PubMed, Taxonomy, LinkOut

```
LOCUS       CIN5_RAT                2019 aa            linear   ROD 15-DEC-1998
DEFINITION  SODIUM CHANNEL PROTEIN, CARDIAC MUSCLE ALPHA-SUBUNIT.
ACCESSION   P15389
PID         g116452
VERSION     P15389  GI:116452
DBSOURCE    swissprot: locus CIN5_RAT, accession P15389;
            class: standard.
            created: Apr 1, 1990.
            sequence updated: Apr 1, 1990.
            annotation updated: Dec 15, 1998.
            xrefs: gi: 206857, gi: 206858, gi: 112312
            xrefs (non-sequence databases): PFAM PF00520, PFAM PF00612
KEYWORDS    Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
            Glycoprotein; Duplication; Multigene family; Phosphorylation.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (residues 1 to 2019)
  AUTHORS   Rogart,R.B., Cribbs,L.L., Muglia,L.K., Kephart,D.D. and Kaiser,M.W.
  TITLE     Molecular cloning of a putative tetrodotoxin-resistant rat heart
            Na+ channel isoform
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 86 (20), 8170-8174 (1989)
  MEDLINE   90046760
   PUBMED   2554302
  REMARK    SEQUENCE FROM N.A.
            TISSUE=HEART
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [FUNCTION] THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
            PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
            CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
            MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
            WHICH NA+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
            GRADIENT. IT IS A TETRODOTOXIN-RESISTANT NA+ CHANNEL ISOFORM.
            [SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN.
            [DOMAIN] THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
            HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
            SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
            CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
            EVERY THIRD POSITION.
            [MISCELLANEOUS] NA+ CHANNELS IN MAMMALIAN CARDIAC MEMBRANE HAVE
            FUNCTIONAL PROPERTIES QUITE DISTINCT FROM NA+ CHANNELS IN NERVE AND
            SKELETAL MUSCLE.
```

```
            [SIMILARITY] TO OTHER SODIUM CHANNEL PROTEINS.
FEATURES             Location/Qualifiers
     source          1..2019
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     gene            1..2019
                     /gene="SCN5A"
     Protein         1..2019
                     /gene="SCN5A"
                     /product="SODIUM CHANNEL PROTEIN, CARDIAC MUSCLE
                     ALPHA-SUBUNIT"
     Region          128..151
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT I (POTENTIAL)."
     Region          160..179
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT I (POTENTIAL)."
     Region          193..211
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT I (POTENTIAL)."
     Site            215
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          218..237
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT I (POTENTIAL)."
     Region          254..277
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT I (POTENTIAL)."
     Site            284
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            289
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            292
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            319
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            329
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          391..416
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT I (POTENTIAL)."
     Site            549
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            593
                     /gene="SCN5A"
```

```
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          713..737
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT II (POTENTIAL)."
     Site            741
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          749..772
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT II (POTENTIAL)."
     Region          781..800
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT II (POTENTIAL)."
     Site            804
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          807..826
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT II (POTENTIAL)."
     Site            842
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          843..863
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT II (POTENTIAL)."
     Site            865
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          917..942
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT II (POTENTIAL)."
     Site            949
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          1203..1226
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT III (POTENTIAL)."
     Region          1240..1265
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT III (POTENTIAL)."
     Region          1272..1293
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT III (POTENTIAL)."
     Region          1298..1319
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT III (POTENTIAL)."
     Region          1339..1361
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
```

```
                     /note="S5 OF REPEAT III (POTENTIAL)."
     Site            1367
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            1376
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            1382
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Site            1390
                     /gene="SCN5A"
                     /site_type="glycosylation"
                     /note="POTENTIAL."
     Region          1446..1472
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT III (POTENTIAL)."
     Region          1526..1549
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT IV (POTENTIAL)."
     Region          1561..1584
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT IV (POTENTIAL)."
     Region          1591..1614
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT IV (POTENTIAL)."
     Region          1625..1646
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT IV (POTENTIAL)."
     Region          1662..1684
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT IV (POTENTIAL)."
     Region          1750..1774
                     /gene="SCN5A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT IV (POTENTIAL)."
ORIGIN
        1 manlllprgt ssfrrftres laaiekrmae kqarggsats qesreglqee eaprpqldlq
       61 askklpdlyg nppreligep ledldpfyst qktfivlnkg ktifrfsatn alyvlspfhp
      121 vrraavkilv hslfsmlimc tiltncvfma qhdpppwtky veytftaiyt feslvkilar
      181 gfclhaftfl rdpwnwldfs vivmayttef vdlgnvsalr tfrvlralkt isvisglkti
      241 vgaliqsvkk ladvmvltvf clsvfaligl qlfmgnlrhk cvrnftelng tngsveadgl
      301 vwnsldvyln dpanyllkng ttdvllcgns sdagtcpegy rclkagenpd hgytsfdsfa
      361 waflalfrlm tqdcwerlyq qtlrsagkiy miffmlvifl gsfylvnlil avvamayeeq
      421 nqatiaetee kekrfqeame mlkkehealt irgvdtvsrs slemsplapv tnherkskrr
      481 krlssgtedg gddrlpksds edgpralnql slthglsrts mrprssrgsi ftfrrrdqgs
      541 eadfaddens tageseshrt sllvpwplrh psaqgqpgpg asapgyvlng krnstvdcng
      601 vvsllgagda eatspgsyll rpmvldrppd tttpseepgg pqmltpqapc adgfeepgar
      661 qralsavsvl tsaleelees hrkcppcwnr faqhyliwec cplwmsikqk vkfvvmdpfa
      721 dltitmcivl ntlfmalehy nmtaefeeml qvgnlvftgi ftaemtfkii aldpyyyfqq
      781 gwnifdsiiv ilslmelgls rmgnlsvlrs frllrvfkla kswptlntli kiignsvgal
      841 gnltlvlaii vfifavvgmq lfgknyselr hrisdsgllp rwhmmdffha fliifrilcg
      901 ewietmwdcm evsgqslcll vfllvmvign lvvlnlflal llssfsadnl tapdedgemn
      961 nlqlalariq rglrfvkrtt wdfccgilrr rpkkpaalat hsqlpscita prsppppeve
     1021 kvpparketr feedkrpgqg tpgdsepvcv piavaesdte dqeedeensl gteeesskqe
     1081 sqvvsgghep yqeprawsqv settsseaga stsqadwqqe qktepqapgc getpedsyse
```

```
     1141 gstadmtnta dlleqipdlg edvkdpedcf tegcvrrcpc cmvdttqspg kvwwrlrktc
     1201 yrivehswfe tfiifmills sgalafediy leerktikvl leyadkmfty vfvlemllkw
     1261 vaygfkkyft nawcwldfli vdvslvslva ntlgfaemgp ikslrtlral rplralsrfe
     1321 gmrvvvvnalv gaipsimnvl lvclifwlif simgvnlfag kfgrcinqte gdlplnytiv
     1381 nnksecesfn vtgelywtkv kvnfdnvgag ylallqvatf kgwmdimyaa vdsrgyeeqp
     1441 qwednlymyi yfvvfiifgs fftlnlfigv iidnfnqqkk klggqdifmt eeqkkyynam
     1501 kklgskkpqk piprplnkyq gfifdivtkq afdvtimfli clnmvtmmve tddqspekvn
     1561 ilakinllfv aiftgecivk maalrhyyft nswnifdfvv vilsivgtvl sdiiqkyffs
     1621 ptlfrvirla rigrilrlir gakgirtllf almmslpalf niglllflvm fiysifgman
     1681 fayvkweagi ddmfnfqtfa nsmlclfqit tsagwdglls pilntgppyc dpnlpnsngs
     1741 rgncgspavg ilffttyiii sflivvnmyi aiilenfsva teesteplse ddfdmfyeiw
     1801 ekfdpeatqf ieylalsdfa dalseplria kpnqislinm dlpmvsgdri hcmdilfaft
     1861 krvlgesgem dalkiqmeek fmaanpskis yepitttlrr kheevsatvi qrafrrhllq
     1921 rsvkhasflf rqqaggsgls dedaperegl iaymmngnfs rrsaplssss isstsfppsy
     1981 dsvtratsdn lpvrasdysr sedladfpps pdrdresiv
//
```

Revised: October 24, 2001.

1: Q99250. Sodium channel pr...[gi:6648080]

BLink, OMIM, Related Sequences, PubMed, Taxonomy, LinkOut

```
LOCUS       CIN2_HUMAN              2005 aa            linear   PRI 01-MAR-2002
DEFINITION  Sodium channel protein, brain II alpha subunit.
ACCESSION   Q99250
PID         g6648080
VERSION     Q99250  GI:6648080
DBSOURCE    swissprot: locus CIN2_HUMAN, accession Q99250;
            class: standard.
            extra accessions:Q14472,created: Jun 1, 1994.
            sequence updated: May 30, 2000.
            annotation updated: Mar 1, 2002.
            xrefs: gi: 456678, gi: 457879, gi: 3075512, gi: 3075513, gi: 36419,
            gi: 36420, gi: 338282, gi: 179560, gi: 12750754, gi: 418893
            xrefs (non-sequence databases): MIM 182390, InterPro IPR001682,
            InterPro IPR002111, InterPro IPR000048, InterPro IPR000636,
            InterPro IPR001696, Pfam PF00520, Pfam PF00612, PRINTS PR00170,
            SMART SM00015, PROSITE PS50096
KEYWORDS    Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
            Glycoprotein; Repeat; Multigene family.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (residues 1 to 2005)
  AUTHORS   Ahmed,C.M., Ware,D.H., Lee,S.C., Patten,C.D., Ferrer-Montiel,A.V.,
            Schinder,A.F., McPherson,J.D., Wagner-Mcpherson,C.B., Wasmuth,J.J.,
            Evans,G.A. and Montal,M.
  TITLE     Primary structure, chromosomal localization, and functional
            expression of a voltage-gated sodium channel from human brain
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 89 (17), 8220-8224 (1992)
  MEDLINE   92390418
  REMARK    SEQUENCE FROM N.A.
            TISSUE=Brain
REFERENCE   2  (residues 1 to 2005)
  AUTHORS   Lu,C.-M., Eichelberger,J.S., Beckman,M.L., Schade,S.D. and
            Brown,G.B.
  TITLE     Direct Submission
  JOURNAL   Submitted (~APR-1998)
  REMARK    SEQUENCE OF 1-89 FROM N.A.
REFERENCE   3  (residues 1 to 2005)
  AUTHORS   Lu,C.M., Han,J., Rado,T.A. and Brown,G.B.
  TITLE     Differential expression of two sodium channel subtypes in human
            brain
  JOURNAL   FEBS Lett. 303 (1), 53-58 (1992)
  MEDLINE   92275082
  REMARK    SEQUENCE OF 1702-2005 FROM N.A.
            TISSUE=Brain
REFERENCE   4  (residues 1 to 2005)
  AUTHORS   Han,J.A., Lu,C.M., Brown,G.B. and Rado,T.A.
  TITLE     Direct amplification of a single dissected chromosomal segment by
            polymerase chain reaction: a human brain sodium channel gene is on
```

```
            chromosome 2q22-q23
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (2), 335-339 (1991)
  MEDLINE   91110524
  REMARK    SEQUENCE OF 1702-1772 FROM N.A.
COMMENT     On Dec 30, 1999 this sequence version replaced gi:544037.
            ---------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------.
            [FUNCTION] THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
            PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
            CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
            MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
            WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
            GRADIENT.
            [SUBUNIT] THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND
            2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
            [SUBCELLULAR LOCATION] Integral membrane protein.
            [DOMAIN] THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
            HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
            SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
            CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
            EVERY THIRD POSITION.
            [SIMILARITY] TO OTHER SODIUM CHANNEL PROTEINS.
            [SIMILARITY] CONTAINS 1 IQ DOMAIN.
FEATURES             Location/Qualifiers
     source          1..2005
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     gene            1..2005
                     /gene="SCN2A1"
                     /note="SCN2A; NAC2"
     Protein         1..2005
                     /gene="SCN2A1"
                     /product="Sodium channel protein, brain II alpha subunit"
     Region          111..456
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="I."
     Region          125..148
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT I."
     Region          157..176
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT I."
     Region          190..208
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT I."
     Site            212
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          215..234
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT I."
     Region          251..274
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
```

```
                     /note="S5 OF REPEAT I."
     Site            285
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            291
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            297
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            303
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            308
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            340
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          402..427
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT I."
     Site            604
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            624
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          741..1013
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="II."
     Region          754..778
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT II."
     Region          790..813
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT II."
     Region          822..841
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT II."
     Region          848..867
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT II."
     Site            883
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          884..904
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT II."
```

```
     Region          958..983
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT II."
     Site            1055
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1072
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1136
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1190..1504
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="III."
     Region          1204..1227
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT III."
     Region          1241..1266
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT III."
     Region          1273..1294
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT III."
     Region          1299..1320
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT III."
     Region          1340..1367
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT III."
     Site            1368
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1382
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1393
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1447..1473
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT III."
     Region          1513..1811
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="IV."
     Region          1527..1550
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT IV."
     Region          1562..1585
```

```
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT IV."
     Region          1592..1615
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT IV."
     Region          1626..1647
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT IV."
     Region          1663..1685
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT IV."
     Region          1752..1776
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT IV."
     Region          1768
                     /gene="SCN2A1"
                     /region_name="Conflict"
                     /note="L -> V (IN REF. 3 AND 4)."
     Site            1778
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1905..1934
                     /gene="SCN2A1"
                     /region_name="Domain"
                     /note="IQ."
     Region          1990
                     /gene="SCN2A1"
                     /region_name="Conflict"
                     /note="K -> R (IN REF. 3)."
     Region          1995..2004
                     /gene="SCN2A1"
                     /region_name="Conflict"
                     /note="DKGKDIRESK -> VEKIKKPFT (IN REF. 3)."
ORIGIN
        1 maqsvlvppg pdsfrfftre slaaieqria eekakrpkqe rkdeddengp kpnsdleagk
       61 slpfiygdip pemvsvpled ldpyyinkkt fivlnkgkai srfsatpaly iltpfnpirk
      121 laikilvhsl fnmlimctil tncvfmtmsn ppdwtknvey tftgiytfes likilargfc
      181 ledftflrdp wnwldftvit fayvtefvdl gnvsalrtfr vlralktisv ipglktivga
      241 liqsvkklsd vmiltvfcls vfaliglqlf mgnlrnkclq wppdnssfei nitsffnnsl
      301 dgngttfnrt vsifnwdeyi edkshfyfle gqndallcgn ssdagqcpeg yicvkagrnp
      361 nygytsfdtf swaflslfrl mtqdfwenly qltlraagkt ymiffvlvif lgsfylinli
      421 lavvamayee qnqatleeae qkeaefqqml eqlkkqqeea qaaaaaasae srdfsgaggi
      481 gvfsesssva sklssksеke lknrrkkkkq keqsgeeekn drvlksesed sirrkgfrfs
      541 legsrltyek rfssphqsll sirgslfspr rnsraslfsf rgrakdigse ndfaddehst
      601 fedndsrrds lfvphrhger rhsnvsqasr asrvlpilpm ngkmhsavdc ngvvslvggp
      661 stltsagqll pegtttetei rkrrsssyhv smdlledpts rqramsiasi ltntmeelee
      721 srqkcppcwy kfanmcliwd cckpwlkvkh lvnlvvmdpf vdlaiticiv lntlfmameh
      781 ypmteqfssv lsvgnlvftg iftaemflki iamdpyyyfq egwnifdgfi vslslmelgl
      841 anveglsvlr sfrllrvfkl akswptlnml ikiignsvga lgnltlvlai ivfifavvgm
      901 qlfgksykec vckisndcel prwhmhdffh sflivfrvlc gewietmwdc mevagqtmcl
      961 tvfmmvmvig nlvvlnlfla lllssfssdn laatdddnem nnlqiavgrm qkgidfvkrk
     1021 irefiqkafv rkqkaldeik pledlnnkkd scisnhttie igkdlnylkd gngttsgigs
     1081 svekyvvdes dymsfinnps ltvtvpiavg esdfenlnte efssesdmee skeklnatss
     1141 segstvdiga paegeqpeve peeslepeac ftedcvrkfk ccqisieegk gklwwnlrkt
     1201 cykivehnwf etfivfmill ssgalafedi yieqrktikt mleyadkvft yifilemllk
     1261 wvaygfqvyf tnawcwldfl ivdvslvslt analgyselg aikslrtlra lrplralsrf
     1321 egmravvnal lgaipsimnv llvclifwli fsimgvnlfa gkfyhcinyt tgemfdvsvv
     1381 nnyseckali esnqtarwkn vkvnfdnvgl gylsllqvat fkgwmdimya avdsrnvelq
     1441 pkyednlymy lyfvifiifg sfftlnlfig viidnfnqqk kkfggqdifm teeqkkyyna
```

```
     1501 mkklgskkpq kpiprpankf qgmvfdfvtk qvfdisimil iclnmvtmmv etddqsqemt
     1561 nilywinlvf ivlftgecvl klislryyyf tigwnifdfv vvilsivgmf laeliekyfv
     1621 sptlfrvirl arigrilrli kgakgirtll falmmslpal fnigllflv mfiyaifgms
     1681 nfayvkrevg iddmfnfetf gnsmiclfqi ttsagwdgll apilnsgppd cdpdkdhpgs
     1741 svkgdcgnps vgifffvsyi iisflvvlnm yiavilenfs vateesaepl seddfemfye
     1801 vwekfdpdat qfiefaklsd fadaldppll iakpnkvqli amdlpmvsgd rihcldilfa
     1861 ftkrvlgesg emdalriqme erfmasnpsk vsyepitttl krkqeevsai iiqrayrryl
     1921 lkqkvkkvss iykkdkgkec dgtpikedtl idklnenstp ektdmtpstt sppsydsvtk
     1981 pekekfekdk sekedkgkdi reskk
//
```

Revised: October 24, 2001.

1: P04775. Sodium channel pr...[gi:116448] BLink, Related Sequences, PubMed, Taxonomy, LinkOut

```
LOCUS       CIN2_RAT                2005 aa            linear   ROD 16-OCT-2001
DEFINITION  Sodium channel protein, brain II alpha subunit.
ACCESSION   P04775
PID         g116448
VERSION     P04775  GI:116448
DBSOURCE    swissprot: locus CIN2_RAT, accession P04775;
            class: standard.
            created: Aug 13, 1987.
            sequence updated: Aug 13, 1987.
            annotation updated: Oct 16, 2001.
            xrefs: gi: 57214, gi: 57215, gi: 92753
            xrefs (non-sequence databases): InterPro IPR002111, InterPro
            IPR000636, InterPro IPR001682, InterPro IPR000048, InterPro
            IPR001696, Pfam PF00520, Pfam PF00612, PRINTS PR00170, SMART
            SM00015, PROSITE PS50096
KEYWORDS    Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
            Glycoprotein; Repeat; Multigene family.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (residues 1 to 2005)
  AUTHORS   Noda,M., Ikeda,T., Kayano,T., Suzuki,H., Takeshima,H., Kurasaki,M.,
            Takahashi,H. and Numa,S.
  TITLE     Existence of distinct sodium channel messenger RNAs in rat brain
  JOURNAL   Nature 320 (6058), 188-192 (1986)
  MEDLINE   86146901
  REMARK    SEQUENCE FROM N.A.
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [FUNCTION] THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
            PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
            CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
            MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
            WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
            GRADIENT.
            [SUBUNIT] THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND
            2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
            [SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN.
            [DOMAIN] THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
            HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
            SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
            CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
            EVERY THIRD POSITION.
            [SIMILARITY] TO OTHER SODIUM CHANNEL PROTEINS.
```

```
            [SIMILARITY] CONTAINS 1 IQ DOMAIN.
FEATURES             Location/Qualifiers
     source          1..2005
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     gene            1..2005
                     /gene="SCN2A1"
                     /note="SCN2A"
     Protein         1..2005
                     /gene="SCN2A1"
                     /product="Sodium channel protein, brain II alpha subunit"
     Region          111..456
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="I."
     Region          125..148
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT I."
     Region          157..176
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT I."
     Region          190..208
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT I."
     Site            212
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          215..234
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT I."
     Region          251..274
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT I."
     Site            285
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            291
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            297
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            303
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            308
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            340
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          402..427
                     /gene="SCN2A1"
```

```
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT I."
     Site            604
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            624
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          741..1013
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="II."
     Region          754..778
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT II."
     Region          790..813
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT II."
     Region          822..841
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT II."
     Region          848..867
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT II."
     Site            883
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          884..904
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT II."
     Region          958..983
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT II."
     Site            1055
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1072
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1136
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1190..1504
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="III."
     Region          1204..1227
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT III."
     Region          1241..1266
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
```

```
                     /note="S2 OF REPEAT III."
     Region          1273..1294
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT III."
     Region          1299..1320
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT III."
     Region          1340..1367
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT III."
     Site            1368
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1382
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1393
                     /gene="SCN2A1"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1447..1473
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT III."
     Region          1513..1811
                     /gene="SCN2A1"
                     /region_name="Repetitive region"
                     /note="IV."
     Region          1527..1550
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT IV."
     Region          1562..1585
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT IV."
     Region          1592..1615
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT IV."
     Region          1626..1647
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT IV."
     Region          1663..1685
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT IV."
     Region          1752..1776
                     /gene="SCN2A1"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT IV."
     Region          1905..1934
                     /gene="SCN2A1"
                     /region_name="Domain"
                     /note="IQ."
ORIGIN
        1 marsvlvppg pdsfrfftre slaaieqria eekakrpkqe rkdeddengp kpnsdleagk
       61 slpfiygdip pemvsepled ldpyyinkkt fivlnkgkai srfsatsaly iltpfnpirk
      121 laikilvhsl fnvlimctil tncvfmtmsn ppdwtknvey tftgiytfes likilargfc
```

```
     181 ledftflrnp wnwldftvit fayvtefvnl gnvsalrtfr vlralktisv ipglktivga
     241 liqsvkklsd vmiltvfcls vfaliglqlf mgnlrnkclq wppdnstfei nitsffnnsl
     301 dwngtafnrt vnmfnwdeyi edkshfyfle gqndallcgn ssdagqcpeg yicvkagrnp
     361 nygytsfdtf swaflslfrl mtqdfwenly qltlraagkt ymiffvlvif lgsfylinli
     421 lavvamayee qnqatleeae qkeaefqqml eqlkkqqeea qaaaaaasae srdfsgaggi
     481 gvfsesssva sklsskseke lknrrkkkkq keqageeeke davrksased sirkkgfqfs
     541 legsrltyek rfssphqsll sirgslfspr rnsraslfnf kgrvkdigse ndfaddehst
     601 fedndsrrds lfvphrhger rpsnvsqasr asrgiptlpm ngkmhsavdc ngvvslvggp
     661 saltspvgql lpegtttete irkrrsssyh vsmdlledps rqramsmasi ltntmeelee
     721 srqkcppcwy kfanmcliwd cckpwlkvkh vvnlvvmdpf vdlaiticiv lntlfmameh
     781 ypmteqfssv lsvgnlvftg iftaemflki iamdpyyyfq egwnifdgfi vslslmelgl
     841 anveglsvlr sfrllrvfkl akswptlnml ikiignsvga lgnltlvlai ivfifavvgm
     901 qlfgksykec vckisndcel prwhmhhffh sflivfrvlc gewietmwdc mevagqtmcl
     961 tvfmmvmvig nlvvlnlfla lllssfssdn laatdddnem nnlqiavgrm qkgidfvkrk
    1021 irefiqkafv rkqkaldeik pledlnnkkd scisnhttie igkdlnylkd gngttsgigs
    1081 svekyvvdes dymsfinnps ltvtvpialg esdfenlnte efssesdmee skeklnatss
    1141 segstvdiga paegeqpeae peeslepeac ftedcvrkfk ccqisieegk gklwwnlrkt
    1201 cykivehnwf etfivfmill ssgalafedi yieqrktikt mleyadkvft yifilemllk
    1261 wvaygfqmyf tnawcwldfl ivdvslvslt analgyselg aikslrtlra lrplralsrf
    1321 egmrvvvnal lgaipsimnv llvclifwli fsimgvnlfa gkfyhcinyt tgemfdvsvv
    1381 nnysecqali esnqtarwkn vkvnfdnvgl gylsllqvat fkgwmdimya avdsrnvelq
    1441 pkyednlymy lyfvifiifg sfftlnlfig viidnfnqqk kkfggqdifm teeqkkyyna
    1501 mkklgskkpq kpiprpankf qgmvfdfvtk qvfdisimil iclnmvtmmv etddqsqemt
    1561 nilywinlvf ivlftgecvl klislrhyyf tigwnifdfv vvilsivgmf laeliekyfv
    1621 sptlfrvirl arigrilrli kgakgirtll falmmslpal fniglllflv mfiyaifgms
    1681 nfayvkrevg iddmfnfetf gnsmiclfqi ttsagwdgll apilnsgppd cdpekdhpgs
    1741 svkgdcgnps vgifffvsyi iisflvvvnm yiavilenfs vateesaepl seddfemfye
    1801 vwekfdpdat qfiefcklsd faaaldppll iakpnkvqli amdlpmvsgd rihcldilfa
    1861 ftkrvlgesg emdalriqme erfmasnpsk vsyepitttl krkqeevsai viqrayrryl
    1921 lkqkvkkvss iykkdkgked egtpikedii tdklnenstp ektdvtpstt sppsydsvtk
    1981 pekekfekdk sekedkgkdi reskk
//
```

Revised: October 24, 2001.

1: X92184. R.norvegicus mRNA...[gi:1209466] Related Sequences, Protein, PubMed, Taxonomy, LinkOut

```
LOCUS       RNSNS                   6524 bp    mRNA    linear   ROD 29-FEB-1996
DEFINITION  R.norvegicus mRNA for voltage-gated sodium channel (SNS).
ACCESSION   X92184
VERSION     X92184.1  GI:1209466
KEYWORDS    SNS gene; voltage-gated sodium channel.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 6524)
  AUTHORS   Akopian,A.N., Sivilotti,L. and Wood,J.N.
  TITLE     A tetrodotoxin-resistant voltage-gated sodium channel expressed by
            sensory neurons
  JOURNAL   Nature 379 (6562), 257-262 (1996)
  MEDLINE   96138382
REFERENCE   2  (bases 1 to 6524)
  AUTHORS   Wood,J.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-OCT-1995) J.N. Wood, University College, Dept of
            Anatomy & Developmental Biology, Gower Street, London WC1E 6BT, UK
FEATURES             Location/Qualifiers
     source          1..6524
                     /organism="Rattus norvegicus"
                     /sub_strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /cell_type="neurons"
                     /tissue_type="DRG"
                     /dev_stage="neonatal"
     gene            204..6077
                     /gene="SNS"
     CDS             204..6077
                     /gene="SNS"
                     /codon_start=1
                     /product="volatage-gated sodium channel"
                     /protein_id="CAA63095.1"
                     /db_xref="GI:1209467"
                     /db_xref="SPTREMBL:Q63554"
                     /translation="MELPFASVGTTNFRRFTPESLAEIEKQIAAHRAAKKARTKHRGQ
                     EDKGEKPRPQLDLKDCNQLPKFYGELPAELVGEPLEDLDPFYSTHRTFMVLNKSRTIS
                     RFSATWALWLFSPFNLIRRTAIKVSVHSWFSIFITITILVNCVCMTRTDLPEKVEYVF
                     TVIYTFEALIKILARGFCLNEFTYLRDPWNWLDFSVITLAYVGAAIDLRGISGLRTFR
                     VLRALKTVSVIPGLKVIVGALIHSVRKLADVTILTVFCLSVFALVGLQLFKGNLKNKC
                     IRNGTDPHKADNLSSEMAEYIFIKPGTTDPLLCGNGSDAGHCPGGYVCLKTPDNPDFN
                     YTSFDSFAWAFLSLFRLMTQDSWERLYQQTLRASGKMYMVFFVLVIFLGSFYLVNLIL
                     AVVTMAYEEQSQATIAEIEAKEKKFQEALEVLQKEQEVLEALGIDTTSLQSHSGSPLA
                     SKNANERRPRVKSRVSEGSTDDNRSPQSDPYNQRRMSFLGLSSGRRRASHGSVFHFRA
                     PSQDISFPDGITPDDGVFHGDQESRRGSILLGRGAGQTGPLPRSPLPQSPNPGRRHGE
                     EGQLGVPTGELTAGAPEGPALHTTGQKSFLSAGYLNEPFRAQRAMSVVSIMTSVIEEL
                     EESKLKCPPCLISFAQKYLIWECCPKWRKFKMALFELVTDPFAELTITLCIVVNTVFM
                     AMEHYPMTDAFDAMLQAGNIVFTVFFTMEMAFKIIAFDPYYYFQKKWNIFDCVIVTVS
```

LLELSASKKGSLSVLRTLRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTFILAIIV
FIFALVGKQLLSEDYGCRKDGVSVWNGEKLRWHMCDFFHSFLVVFRILCGEWIENMWV
CMEVSQKSICLILFLTVMVLGNLVVLNLFIALLLNSFSADNLTAPEDDGEVNNLQLAL
ARIQVLGHRASRAIASYISSHCRFHWPKVETQLGMKPPLTSSEAKNHIATDAVSAAVG
NLTKPALSSPKENHGDFITDPNVWVSVPIAEGESDLDELEEDMEQASQSSWQEEDPKG
QQEQLPQVQKCENHQAARSPASMMSSEDLAPYLGESWKRKDSPQVPAEGVDDTSSSEG
STVDCPDPEEILRKIPELADDLDEPDDCFTEGCTRRCPCCNVNTSKSPWATGWQVRKT
CYRIVEHSWFESFIIFMILLSSGALAFEDNYLEEKPRVKSVLEYTDRVFTFIFVFEML
LKWVAYGFKKYFTNAWCWLDFLIVNISLTSLIAKILEYSDVASIKALRTLRALRPLRA
LSRFEGMRVVVDALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFSKCVDTRNNPF
SNVNSTMVNNKSECHNQNSTGHFFWVNVKVNFDNVAMGYLALLQVATFKGWMDIMYAA
VDSGEINSQPNWENNLYMYLYFVVFIIFGGFFTLNLFVGVIIDNFNQQKKKLGGQDIF
MTEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFVFDIVTRQAFDIIIMVLICLNMIT
MMVETDEQGEEKTKVLGRINQFFVAVFTGECVMKMFALRQYYFTNGWNVFDFIVVILS
IGSLLFSAILKSLENYFSPTLFRVIRLARIGRILRLIRAAKGIRTLLFALMMSLPALF
NIGLLLFLVMFIYSIFGMASFANVVDEAGIDDMFNFKTFGNSMLCLFQITTSAGWDGL
LSPILNTGPPYCDPNLPNSNGSRGNCGSPAVGIIFFTTYIIISFLIVVNMYIAVILEN
FNVATEESTEPLSEDDFDMFYETWEKFDPEATQFIAFSALSDFADTLSGPLRIPKPNQ
NILIQMDLPLVPGDKIHCLDILFAFTKNVLGESGELDSLKTNMEEKFMATNLSKASYE
PIATTLRWKQEDLSATVIQKAYRSYMLHRSLTLSNTLHVPRAEEDGVSLPGEGYITFM
ANSGLPDKSETASATSFPPSYDSVTRGLSDRANINPSSSMQNEDEVAAKEGNSPGPQ"

BASE COUNT 1542 a 1864 c 1660 g 1458 t

ORIGIN

```
      1 tagcttgctt ctgctaatgc taccccaggc ctttagacag agaacagatg gcagatggag
     61 tttcttattg ccatgcgcaa acgctgagcc cacctcatga tcccggaccc catggttttc
    121 agtagacaac ctgggctaag aagagatctc cgaccttata gagcagcaaa gagtgtaaat
    181 tcttccccaa gaagaatgag aagatggagc tccccttttgc gtccgtggga actaccaatt
    241 tcagacggtt cactccagag tcactggcag agatcgagaa gcagattgct gctcaccgcg
    301 cagccaagaa ggccagaacc aagcacagag gacaggagga caagggcgag aagcccaggc
    361 ctcagctgga cttgaaagac tgtaaccagc tgcccaagtt ctatggtgag ctcccagcag
    421 aactggtcgg ggagcccctg gaggacctag acccctttcta cagcacacac cggacattca
    481 tggtgttgaa taaaagcagg accatttcca gattcagtgc cacttgggcc ctgtggctct
    541 tcagtccctt caacctgatc agaagaacag ccatcaaagt gtctgtccat tcctggttct
    601 ccatattcat caccatcact attttggtca actgcgtgtg catgacccga actgatcttc
    661 cagagaaagt cgagtacgtc ttcactgtca tttacacctt cgaggctctg attaagatac
    721 tggcaagagg gttttgtcta aatgagttca cttatcttcg agatccgtgg aactggctgg
    781 acttcagtgt cattaccttg gcgtatgtgg gtgcagcgat agacctccga ggaatctcag
    841 gcctgcggac attccgagtt ctcagagccc tgaaaactgt ttctgtgatc ccaggactga
    901 aggtcatcgt gggagccctg atccactcag tgaggaagct ggccgacgtg actatcctca
    961 cagtcttctg cctgagcgtc ttcgccttgg tgggcctgca gctctttaag gggaacctta
   1021 agaacaaatg catcaggaac ggaacagatc cccacaaggc tgacaacctc tcatctgaaa
   1081 tggcagaata catcttcatc aagcctggta ctacggatcc cttactgtgc ggcaatgggt
   1141 ctgatgctgg tcactgccct ggaggctatg tctgcctgaa aactcctgac aacccggatt
   1201 ttaactacac cagctttgat tcctttgcgt gggcattcct ctcactgttc cgcctcatga
   1261 cgcaggactc ctgggagcgc ctgtaccagc agacactccg ggcttctggg aaaatgtaca
   1321 tggtcttttt cgtgctggtt attttccttg gatcgttcta cctggtcaat ttgatcttgg
   1381 ccgtggtcac catggcgtat gaagagcaga gccaggcaac aattgcagaa atcgaagcca
   1441 aggaaaaaaa gttccaggaa gcccttgagg tgctgcagaa ggaacaggag gtgctggaag
   1501 ccctggggat tgacacgacc tcgctccagt cccacagtgg atcaccctta gcctccaaaa
   1561 acgccaatga gagaagaccc agggtgaaat caagggtgtc agagggctcc acggatgaca
   1621 acaggtcacc ccaatctgac ccttacaacc agcgcaggat gtctttccta ggcctgtctt
   1681 caggaagacg cagggctagc cacggcagtg tgttccactt ccgagcgccc agccaagaca
   1741 tctcatttcc tgacgggatc acccctgatg atggggtctt tcacggagac caggaaagcc
   1801 gtcgaggttc catattgctg ggcaggggtg ctgggcagac aggtccactc cccaggagcc
   1861 cactgcctca gtcccccaac cctggccgta gacatggaga agagggacag ctcggagtgc
   1921 ccactggtga gcttaccgct ggagcgcctg aaggcccggc actgcacact acagggcaga
   1981 agagcttcct gtctgcgggc tacttgaacg aacctttccg agcacagagg gccatgagcg
   2041 ttgtcagtat catgacttct gtcattgagg agcttgaaga gtctaagctg aagtgcccac
   2101 cctgcttgat cagcttcgct cagaagtatc tgatctggga gtgctgcccc aagtggagga
   2161 agttcaagat ggcgctgttc gagctggtga ctgacccctt cgcagagctt accatcaccc
   2221 tctgcatcgt ggtgaacacc gtcttcatgg ccatggagca ctaccccatg accgatgcct
   2281 tcgatgccat gcttcaagcc ggcaacattg tcttcaccgt gtttttcaca atggagatgg
   2341 ccttcaagat cattgccttc gacccctact attacttcca gaagaagtgg aatatcttcg
   2401 actgtgtcat cgtcaccgtg agccttctgg agctgagtgc atccaagaag ggcagcctgt
   2461 ctgtgctccg taccttacgc ttgctgcggg tcttcaagct ggccaagtcc tggcccaccc
```

```
2521 tgaacaccct catcaagatc atcgggaact cagtgggggc cctgggcaac ctgaccttta
2581 tcctggccat catcgtcttc atcttcgccc tggtcggaaa gcagcttctc tcagaggact
2641 acgggtgccg caaggacggc gtctccgtgt ggaacggcga gaagctccgc tggcacatgt
2701 gtgacttctt ccattccttc ctggtcgtct tccgaatcct ctgcggggag tggatcgaga
2761 acatgtgggt ctgcatggag gtcagccaga aatccatctg cctcatcctc ttcttgactg
2821 tgatggtgct gggcaaccta gtggtgctca acctttttcat cgctttactg ctgaactcct
2881 tcagcgcgga caacctcacg gctccagagg atgacgggga ggtgaacaac ttgcagttag
2941 cactggccag gatccaggta cttggccatc gggccagcag ggccatcgcc agttacatca
3001 gcagccactg ccgattccac tggcccaagg tggagaccca gctgggcatg aagcccccac
3061 tcaccagctc agaggccaag aaccacattg ccactgatgc tgtcagtgct gcagtgggga
3121 acctgacaaa gccagctctc agtagcccca aggagaacca cggggacttc atcactgatc
3181 ccaacgtgtg ggtctctgtg cccattgctg agggggaatc tgacctcgac gagctcgagg
3241 aagatatgga gcaggcttcg cagagctcct ggcaggaaga ggaccccaag ggacagcagg
3301 agcagttgcc acaagtccaa aagtgtgaaa accaccaggc agccagaagc ccagcctcca
3361 tgatgtcctc tgaggacctg gctccatacc tgggtgagag ctggaagagg aaggatagcc
3421 ctcaggtccc tgccgaggga gtggatgaca cgagctcctc tgagggcagc acggtggact
3481 gcccggaccc agaggaaatc ctgaggaaga tccccgagct ggcagatgac ctggacgagc
3541 ccgatgactg tttcacagaa ggctgcactc gccgctgtcc ctgctgcaac gtgaatacta
3601 gcaagtctcc ttgggccaca ggctggcagg tgcgcaagac ctgctaccgc atcgtggagc
3661 acagctggtt tgagagtttc atcatcttca tgatcctgct cagcagtgga gcgctggcct
3721 ttgaggataa ctacctggaa gagaaacccc gagtgaagtc cgtgctggag tacactgacc
3781 gagtgttcac cttcatcttc gtctttgaga tgctgctcaa gtgggtagcc tatggcttca
3841 aaaagtattt caccaatgcc tggtgctggc tggacttcct cattgtgaac atctccctga
3901 caagcctcat agcgaagatc cttgagtatt ccgacgtggc gtccatcaaa gcccttcgga
3961 ctctccgtgc cctccgaccg ctgcgggctc tgtctcgatt cgaaggcatg agggtagtgg
4021 tggatgccct cgtgggcgcc atcccctcca tcatgaacgt cctcctcgtc tgcctcatct
4081 tctggctcat cttcagcatc atgggcgtga acctcttcgc cgggaaattt tcgaagtgcg
4141 tcgacaccag aaataaccca ttttccaacg tgaattcgac gatggtgaat aacaagtccg
4201 agtgtcacaa tcaaaacagc accggccact tcttctgggt caacgtcaaa gtcaacttcg
4261 acaacgtcgc tatgggctac ctcgcacttc ttcaggtggc aaccttcaaa ggctggatgg
4321 acataatgta tgcagctgtt gattccggag agatcaacag tcagcctaac tgggagaaca
4381 acttgtacat gtacctgtac ttcgtcgttt tcatcatttt cggtggcttc ttcacgctga
4441 atctctttgt tggggtcata atcgacaact tcaaccaaca gaaaaaaaag ctaggaggcc
4501 aggacatctt catgacagaa gagcagaaga agtactacaa tgccatgaag aagctgggct
4561 ccaagaaacc ccagaagccc atcccacggc ccctgaataa gtaccaaggc ttcgtgtttg
4621 acatcgtgac caggcaagcc tttgacatca tcatcatggt tctcatctgc ctcaacatga
4681 tcaccatgat ggtggagacc gacgagcagg gcgaggagaa gacgaaggtt ctgggcagaa
4741 tcaaccagtt ctttgtggcc gtcttcacgg gcgagtgtgt gatgaagatg ttcgccctgc
4801 gacagtacta cttcaccaac ggctggaacg tgttcgactt catagtggtg atcctgtcca
4861 ttgggagtct gctgttttct gcaatcctta agtcactgga aaactacttc tccccgacgc
4921 tcttccgggt catccgtctg gccaggatcg gccgcatcct caggctgatc cgagcagcca
4981 aggggattcg cacgctgctc ttcgccctca tgatgtccct gcccgccctc ttcaacatcg
5041 gcctcctcct cttcctcgtc atgttcatct actccatctt cggcatggcc agcttcgcta
5101 acgtcgtgga cgaggccggc atcgacgaca tgttcaactt caagaccttt ggcaacagca
5161 tgctgtgcct gttccagatc accacctcgg ccggctggga cggcctcctc agccccatcc
5221 tcaacacggg gcctccctac tgcgacccca acctgcccaa cagcaacggc tcccggggga
5281 actgcgggag cccggcggtg ggcatcatct tcttcaccac ctacatcatc atctccttcc
5341 tcatcgtggt caacatgtac atcgcagtga ttctggagaa cttcaacgta gccaccgagg
5401 agagcacgga gcccctgagc gaggacgact tcgacatgtt ctatgagacc tgggagaagt
5461 tcgacccgga ggccacccag ttcattgcct tttctgccct ctcagacttc gcggacacgc
5521 tctccggccc tcttagaatc cccaaaccca accagaatat attaatccag atggacctgc
5581 cgttggtccc cggggataag atccactgtc tggacatcct ttttgccttc acaaagaacg
5641 tcttgggaga atccggggag ttggactccc tgaagaccaa tatggaagag aagtttatgg
5701 cgaccaatct ctccaaagca tcctatgaac caatagccac caccctccgg tggaagcagg
5761 aagacctctc agccacagtc attcaaaagg cctaccggag ctacatgctg caccgctcct
5821 tgacactctc caacaccctg catgtgccca gggctgagga ggatggcgtg tcacttcccg
5881 gggaaggcta cattacattc atggcaaaca gtggactccc ggacaaatca gaaactgcct
5941 ctgctacgtc tttcccgcca tcctatgaca gtgtcaccag gggcctgagt gaccgggcca
6001 acattaaccc atctagctca atgcaaaatg aagatgaggt cgctgctaag gaaggaaaca
6061 gccctggacc tcagtgaagg cactcaggca tgcacagggc aggttccaat gtctttctct
6121 gctgtactaa ctccttccct ctggaggtgg caccaacctc cagcctccac caatgcatgt
6181 cactggtcat ggtgtcagaa ctgaatgggg acatccttga gaaagccccc accccaatag
6241 gaatcaaaag ccaaggatac tcctccattc tgacgtccct tccgagttcc cagaagatgt
6301 cattgctccc ttctgtttgt gaccagagac gtgattcacc aacttctcgg agccagagac
6361 acatagcaaa gacttttctg ctggtgtcgg gcagtcttag agaagtcacg taggggttgg
```

```
     6421 tactgagaat tagggtttgc atgactgcat gctcacagct gccggacaat acctgtgagt
     6481 cggccattaa aattaatatt tttaaagtta aaaaaaaaaa aaaa
//
```

Revised: October 24, 2001.

1: U53833. Rattus norvegicus...[gi:1280042]

Related Sequences, OMIM, Protein, PubMed, Taxonomy, LinkOut

```
LOCUS       RNU53833                6344 bp    DNA     linear   ROD 20-JUN-1996
DEFINITION  Rattus norvegicus sodium channel PN3 gene, complete cds.
ACCESSION   U53833
VERSION     U53833.1  GI:1280042
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 6344)
  AUTHORS   Sangameswaran,L., Delgado,S.G., Fish,L.M., Koch,B.D., Jakeman,L.B.,
            Stewart,G.R., Sze,P., Hunter,J.C., Eglen,R.M. and Herman,R.C.
  TITLE     Structure and function of a novel voltage-gated,
            tetrodotoxin-resistant sodium channel specific to sensory neurons
  JOURNAL   J. Biol. Chem. 271 (11), 5953-5956 (1996)
  MEDLINE   96198040
   PUBMED   8626372
REFERENCE   2  (bases 1 to 6344)
  AUTHORS   Sangameswaran,L., Delgado,S.G., Fish,L.M. and Herman,R.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-1996) Lakshmi Sangameswaran, Pharmacology,
            Neurobiology Unit, Roche Bioscience, 3401, Hillview Avenue, Palo
            Alto, CA 94304, USA
REFERENCE   3  (bases 1 to 6344)
  AUTHORS   Sangameswaran,L.B., Delgado,S.G., Fish,L.M., Koch,B.D.,
            Jakeman,L.B., Stewart,G.R., Sze,P., Hunter,J.C., Eglen,R.M. and
            Herman,R.C.
  TITLE     Additions and corrections to structure and function of a novel
            voltage-gated, tetrodotoxin-resistant sodium channel specific to
            sensory neurons
  JOURNAL   J. Biol. Chem. 271 (22), 13292-13292 (1996)
FEATURES             Location/Qualifiers
     source          1..6344
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     CDS             23..5893
                     /codon_start=1
                     /product="sodium channel PN3"
                     /protein_id="AAC52619.1"
                     /db_xref="GI:1280043"
                     /translation="MELPFASVGTTNFRRFTPESLAEIEKQIAAHRAAKKARTKHRGQ
                     EDKGEKPRPQLDLKACNQLPKFYGELPAELVGEPLEDLDPFYSTHRTFMVLNKSRTIS
                     RFSATWALWLFSPFNLIRRTAIKVSVHSWFSIFITITILVNCVCMTRTDLPEKVEYVF
                     TVIYTFEALIKILARGFCLNEFTYLRDPWNWLDFSVITLAYVGAAIDLRGISGLRTFR
                     VLRALKTVSVIPGLKVIVGALIHSVRKLADVTILTVFCLSVFALVGLQLFKGNLKNKC
                     IRNGTDPHKADNLSSEMAEYIFIKPGTTDPLLCGNGSDAGHCPGGYVCLKTPDNPDFN
                     YTSFDSFAWAFLSLFRLMTQDSWERLYQQTLRASGKMYMVFFVLVIFLGSFYLVNLIL
                     AVVTMAYEEQSQATIAEIEAKEKKFQEALEVLQKEQEVLAALGIDTTSLQSHSGSPLA
                     SKNANERRPRVKSRVSEGSTDDNRSPQSDPYNQRRMSFLGLSSGRRRASHGSVFHFRA
```

PSQDISFPDGITDDGVFHGDQESRRGSILLGRGAGQTGPLPRSPLPQSPNPGRRHGEE
GQLGVPTGELTAGAPEGPALDTTGQKSFLSAGYLNEPFRAQRAMSVVSIMTSVIEELE
ESKLKCPPCLISFAQKYLIWECCPKWRKFKMALFELVTDPFAELTITLCIVVNTVFMA
MEHYPMTDAFDAMLQAGNIVFTVFFTMEMAFKIIAFDPYYYFQKKWNIFDCVIVTVSL
LELSASKKGSLSVLRTFRLLRVFKLAKSWPTLNTLIKIIGNSVGALGNLTFILAIIVF
IFALVGKQLLSEDYGCRKDGVSVWNGEKLRWHMCDFFHSFLVVFRILCGEWIENMWVC
MEVSQKSICLILFLTVMVLGNLVVLNLFIALLLNSFSADNLTAPEDDGEVNNLQLALA
RIQVLGHRASRAIASYISSHCRFRWPKVETQLGMKPPLTSSEAKNHIATDAVSAAVGN
LTKPALSSPKENHGDFITDPNVWVSVPIAEGESDLDELEEDMEQASQSSWQEEDPKGQ
QEQLPQVQKCENHQAARSPASMMSSEDLAPYLGESWKRKDSPQVPAEGVDDTSSSEGS
TVDCPDPEEILRKIPELADDLDEPDDCFTEGCTRRCPCCNVNTSKSPWATGWQVRKTC
YRIVEHSWFESFIIFMILLSSGALAFEDNYLEEKPRVKSVLEYTDRVFTFIFVFEMLL
KWVAYGFKKYFTNAWCWLDFLIVNISLTSLIAKILEYSDVASIKALRTLRALRPLRAL
SRFEGMRVVVDALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFAGKFSKCVDTRNNPFS
NVNSTMVNNKSECHNQNSTGHFFWVNVKVNFDNVAMGYLALLQVATFKGWMDIMYAAV
DSGEINSQPNWENNLYMYLYFVVFIIFGGFFTLNLFVGVIIDNFNQQKKLGGQDIFM
TEEQKKYYNAMKKLGSKKPQKPIPRPLNKYQGFVFDIVTRQAFDIIIMVLICLNMITM
MVETDEQGEEKTKVLGRINQFFVAVFTGECVMKMFALRQYYFTNGWNVFDFIVVILSI
GSLLFSAILKSLENYFSPTLFRVIRLARIGRILRLIRAAKGIRTLLFALMMSLPALFN
IGLLLFLVMFIYSIFGMASFANVVDEAGIDDMFNFKTFGNSMLCLFQITTSAGWDGLL
SPILNTGPPYCDPNLPNSNGSRGNCGSPAVGIIFFTTYIIISFLIVVNMYIAVILENF
NVATEESTEPLSEDDFDMFYETWEKFDPEATQFIAFSALSDFADTLSGPLRIPKPNQN
ILIQMDLPLVPGDKIHCLDILFAFTKNVLGESGELDSLKTNMEEKFMATNLSKASYEP
IATTLRWKQEDLSATVIQKAYRSYMLHRSLTLSNTLHVPRAEEDGVSLPGEGYVTFMA
NSGLPDKSETASATSFPPSYDSVTRGLSDRANINPSSSMQNEDEVAAKEGNSPGPQ"

BASE COUNT 1487 a 1823 c 1622 g 1412 t

ORIGIN

```
       1 cttccccaag aagaatgaga agatggagct ccccttgcg tccgtgggaa ctaccaattt
      61 cagacggttc actccagagt cactggcaga gatcgagaag cagattgctg ctcaccgcgc
     121 agccaagaag gccagaacca agcacagagg acaggaggac aagggcgaga agcccaggcc
     181 tcagctggac ttgaaagcct gtaaccagct gcccaagttc tatggtgagc tcccagcaga
     241 actggtcggg gagcccctgg aggacctaga ccctttctac agcacacacc ggacattcat
     301 ggtgttgaat aaaagcagga ccatttccag attcagtgcc acttgggccc tgtggctctt
     361 cagtcccttc aacctgatca gaagaacagc catcaaagtg tctgtccatt cctggttctc
     421 catattcatc accatcacta ttttggtcaa ctgcgtgtgc atgacccgaa ctgatcttcc
     481 agagaaagtc gagtacgtct tcactgtcat ttacaccttc gaggctctga ttaagatact
     541 ggcaagaggg ttttgtctaa atgagttcac ttatcttcga gatccgtgga actggctgga
     601 cttcagtgtc attaccttgg cgtatgtggg tgcagcgata gacctccgag gaatctcagg
     661 cctgcggaca ttccgagttc tcagagccct gaaaactgtt tctgtgatcc caggactgaa
     721 ggtcatcgtg ggagccctga tccactcagt gaggaagctg gccgacgtga ctatcctcac
     781 agtcttctgc ctgagcgtct tcgccttggt gggcctgcag ctctttaagg ggaaccttaa
     841 gaacaaatgc atcaggaacg gaacagatcc ccacaaggct gacaacctct catctgaaat
     901 ggcagaatac atcttcatca agcctggtac tacggatccc ttactgtgcg gcaatgggtc
     961 tgatgctggt cactgccctg gaggctatgt ctgcctgaaa actcctgaca acccggattt
    1021 taactacacc agctttgatt cctttgcgtg ggcattcctc tcactgttcc gcctcatgac
    1081 gcaggactcc tgggagcgcc tgtaccagca gacactccgg gcttctggga aaatgtacat
    1141 ggtctttttc gtgctggtta ttttccttgg atcgttctac ctggtcaatt tgatcttggc
    1201 cgtggtcacc atggcgtatg aagagcagag ccaggcaaca attgcagaaa tcgaagccaa
    1261 ggaaaaaaag ttccaggaag cccttgaggt gctgcagaag gaacaggagg tgctggcagc
    1321 cctggggatt gacacgacct cgctccagtc ccacagtgga tcacccttag cctccaaaaa
    1381 cgccaatgag agaagaccca gggtgaaatc aagggtgtca gagggctcca cggatgacaa
    1441 caggtcaccc caatctgacc cttacaacca gcgcaggatg tctttcctag gcctgtcttc
    1501 aggaagacgc agggctagcc acggcagtgt gttccacttc cgagcgccca gccaagacat
    1561 ctcatttcct gacgggatca cggatgatgg ggtctttcac ggagaccagg aaagccgtcg
    1621 aggttccata ttgctgggca ggggtgctgg gcagacaggt ccactcccca ggagcccact
    1681 gcctcagtcc cccaaccctg gccgtagaca tggagaagag ggacagctcg gagtgcccac
    1741 tggtgagctt accgctggag cgcctgaagg cccggcactc gacactacag ggcagaagag
    1801 cttcctgtct gcgggctact tgaacgaacc tttccgagca cagagggcca tgagcgttgt
    1861 cagtatcatg acttctgtca ttgaggagct tgaagagtct aagctgaagt gcccaccctg
    1921 cttgatcagc ttcgctcaga agtatctgat ctgggagtgc tgccccaagt ggaggaagtt
    1981 caagatggcg ctgttcgagc tggtgactga ccccttcgca gagcttacca tcaccctctg
    2041 catcgtggtg aacaccgtct tcatggccat ggagcactac cccatgaccg atgccttcga
    2101 tgccatgctt caagccggca acattgtctt caccgtgttt ttcacaatgg agatggcctt
    2161 caagatcatt gccttcgacc cctactatta cttccagaag aagtggaata tcttcgactg
    2221 tgtcatcgtc accgtgagcc ttctggagct gagcgcatcc aagaagggca gcctgtctgt
```

```
2281 gctccgtacc ttccgcttgc tgcgggtctt caagctggcc aagtcctggc ccaccctgaa
2341 caccctcatc aagatcatcg ggaactccgt gggggccctg ggcaacctga cctttatcct
2401 ggccatcatc gtcttcatct tcgccctggt cggaaagcag cttctctcag aggactacgg
2461 gtgccgcaag gacggcgtct ccgtgtggaa cggcgagaag ctccgctggc acatgtgtga
2521 cttcttccat tccttcctgg tcgtcttccg aatcctctgc ggggagtgga tcgagaacat
2581 gtgggtctgc atggaggtca gccagaaatc catctgcctc atcctcttct tgactgtgat
2641 ggtgctgggc aacctagtgg tgctcaacct tttcatcgct ttactgctga actccttcag
2701 cgcggacaac ctcacggctc cagaggatga cggggaggtg aacaacttgc agttagcact
2761 ggccaggatc caggtacttg gccatcgggc cagcagggcc atcgccagtt acatcagcag
2821 ccactgccga ttccgctggc ccaaggtgga gacccagctg ggcatgaagc ccccactcac
2881 cagctcagag gccaagaacc acattgccac tgatgctgtc agtgctgcag tggggaacct
2941 gacaaagcca gctctcagta gccccaagga gaaccacggg gacttcatca ctgatcccaa
3001 cgtgtgggtc tctgtgccca ttgctgaggg ggaatctgac ctcgacgagc tcgaggaaga
3061 tatggagcag gcttcgcaga gctcctggca ggaagaggac cccaagggac agcaggagca
3121 gttgccacaa gtccaaaagt gtgaaaacca ccaggcagcc agaagcccag cctccatgat
3181 gtcctctgag gacctggctc catacctggg tgagagctgg aagaggaagg atagccctca
3241 ggtccctgcc gagggagtgg atgacacgag ctcctctgag ggcagcacgg tggactgccc
3301 ggacccagag gaaatcctga ggaagatccc cgagctggca gatgacctgg acgagcccga
3361 tgactgtttc acagaaggct gcactcgccg ctgtccctgc tgcaacgtga atactagcaa
3421 gtctccttgg gccacaggct ggcaggtgcg caagacctgc taccgcatcg tggagcacag
3481 ctggtttgag agtttcatca tcttcatgat cctgctcagc agtggagcgc tggcctttga
3541 ggataactac ctggaagaga aaccccgagt gaagtccgtg ctggagtaca ctgaccgagt
3601 gttcaccttc atcttcgtct ttgagatgct gctcaagtgg gtagcctatg gcttcaaaaa
3661 gtatttcacc aatgcctggt gctggctgga cttcctcatt gtgaacatct ccctgacaag
3721 cctcatagcg aagatccttg agtattccga cgtggcgtcc atcaaagccc ttcggactct
3781 ccgtgccctc cgaccgctgc gggctctgtc tcgattcgaa ggcatgaggg tagtggtgga
3841 tgccctcgtg ggcgccatcc cctccatcat gaacgtcctc ctcgtctgcc tcatcttctg
3901 gctcatcttc agcatcatgg gcgtgaacct cttcgccggg aaattttcga agtgcgtcga
3961 caccagaaat aacccatttt ccaacgtgaa ttcgacgatg gtgaataaca agtccgagtg
4021 tcacaatcaa aacagcaccg gccacttctt ctgggtcaac gtcaaagtca acttcgacaa
4081 cgtcgctatg ggctacctcg cacttcttca ggtggcaacc ttcaaaggct ggatggacat
4141 aatgtatgca gctgttgatt ccggagagat caacagtcag cctaactggg agaacaactt
4201 gtacatgtac ctgtacttcg tcgttttcat cattttcggt ggcttcttca cgctgaatct
4261 ctttgttggg gtcataatcg acaacttcaa ccaacagaaa aaaaagctag gaggccagga
4321 catcttcatg acagaagagc agaagaagta ctacaatgcc atgaagaagc tgggctccaa
4381 gaaaccccag aagcccatcc cacggcccct gaataagtac caaggcttcg tgtttgacat
4441 cgtgaccagg caagcctttg acatcatcat catggttctc atctgcctca acatgatcac
4501 catgatggtg gagaccgacg agcagggcga ggagaagacg aaggttctgg gcagaatcaa
4561 ccagttcttt gtggccgtct tcacgggcga gtgtgtgatg aagatgttcg ccctgcgaca
4621 gtactacttc accaacggct ggaacgtgtt cgacttcata gtggtgatcc tgtccattgg
4681 gagtctgctg ttttctgcaa tccttaagtc actggaaaac tacttctccc cgacgctctt
4741 ccgggtcatc cgtctggcca ggatcggccg catcctcagg ctgatccgag cagccaaggg
4801 gattcgcacg ctgctcttcg ccctcatgat gtccctgccc gccctcttca acatcggcct
4861 cctcctcttc ctcgtcatgt tcatctactc catcttcggc atggccagct tcgctaacgt
4921 cgtggacgag gccggcatcg acgacatgtt caacttcaag acctttggca acagcatgct
4981 gtgcctgttc cagatcacca cctcggccgg ctgggacggc ctcctcagcc ccatcctcaa
5041 cacggggcct ccctactgcg accccaacct gcccaacagc aacggctccc gggggaactg
5101 cgggagcccg gcggtgggca tcatcttctt caccacctac atcatcatct ccttcctcat
5161 cgtggtcaac atgtacatcg cagtgattct ggagaacttc aacgtggcca ccgaggagag
5221 cacggagccc ctgagcgagg acgacttcga catgttctat gagacctggg agaagttcga
5281 cccggaggcc acccagttca ttgccttttc tgccctctca gacttcgcgg acacgctctc
5341 cggccctctt agaatcccca aacccaacca gaatatatta atccagatgg acctgccgtt
5401 ggtccccggg gataagatcc actgtctgga catccttttt gccttcacaa agaacgtctt
5461 gggagaatcc ggggagttgg actccctgaa gaccaatatg gaagagaagt ttatggcgac
5521 caatctctcc aaagcatcct atgaaccaat agccaccacc ctccggtgga agcaggaaga
5581 cctctcagcc acagtcattc aaaaggccta ccggagctac atgctgcacc gctccttgac
5641 actctccaac accctgcatg tgcccagggc tgaggaggat ggcgtgtcac ttcccgggga
5701 aggctacgtt acattcatgg caaacagtgg actcccggac aaatcagaaa ctgcctctgc
5761 tacgtctttc ccgccatcct atgacagtgt caccaggggc ctgagtgacc gggccaacat
5821 taacccatct agctcaatgc aaaatgaaga tgaggtcgct gctaaggaag gaaacagccc
5881 tggacctcag tgaaggcact caggcatgca cagggcaggt tccaatgtct ttctctgctg
5941 tgctaactcc ttccctctgg aggtggcacc aacctccagc ctccaccaat gcatgtcact
6001 ggtcatggtg tcagaactga atggggacat ccttgagaaa gcccccaccc caataggaat
6061 caaaagccaa ggatactcct ccattctgac gtcccttccg agttcccaga agatgtcatt
6121 gctcccttct gtttgtgacc agagacgtga ttcaccaact tctcggagcc agagacacat
```

```
     6181 accaaagact tttctgctgg tgtcgggcag tcttagagaa gtcacgtagg ggttggcact
     6241 gagaattagg gtttgcatgc ctgcatgctc acagctgccg gacaatacct gtgagtcggc
     6301 cattaaaatt aatattttta aagttaaaaa aaaaaaaaaa aaaa
//
```

Revised: October 24, 2001.

1: P08104. Sodium channel pr...[gi:116449] BLink, Related Sequences, PubMed, Taxonomy, LinkOut

LOCUS CIN3_RAT 1951 aa linear ROD 16-OCT-2001
DEFINITION Sodium channel protein, brain III alpha subunit (Voltage-gated sodium channel subtype III).
ACCESSION P08104
PID g116449
VERSION P08104 GI:116449
DBSOURCE swissprot: locus CIN3_RAT, accession P08104;
class: standard.
created: Aug 1, 1988.
sequence updated: Aug 1, 1988.
annotation updated: Oct 16, 2001.
xrefs: gi: 57210, gi: 57211, gi: 92754
xrefs (non-sequence databases): InterPro IPR002111, InterPro IPR000636, InterPro IPR001682, InterPro IPR000048, InterPro IPR001696, Pfam PF00520, Pfam PF00612, PRINTS PR00170, SMART SM00015
KEYWORDS Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Repeat; Multigene family.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (residues 1 to 1951)
AUTHORS Kayano,T., Noda,M., Flockerzi,V., Takahashi,H. and Numa,S.
TITLE Primary structure of rat brain sodium channel III deduced from the cDNA sequence
JOURNAL FEBS Lett. 228 (1), 187-194 (1988)
MEDLINE 88137594
REMARK SEQUENCE FROM N.A.
STRAIN=WISTAR
COMMENT ----------
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute.
The original entry is available from http://www.expasy.ch/sprot and http://www.ebi.ac.uk/sprot
----------.
[FUNCTION] THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.
[SUBUNIT] THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND 2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
[SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN.
[DOMAIN] THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5 HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT

```
            EVERY THIRD POSITION.
            [SIMILARITY] TO OTHER SODIUM CHANNEL PROTEINS.
            [SIMILARITY] CONTAINS 1 IQ DOMAIN.
FEATURES             Location/Qualifiers
     source          1..1951
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     gene            1..1951
                     /gene="SCN3A"
     Protein         1..1951
                     /gene="SCN3A"
                     /product="Sodium channel protein, brain III alpha subunit"
     Region          124..147
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT I."
     Region          156..175
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT I."
     Region          189..207
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT I."
     Site            211
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          214..233
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT I."
     Region          249..273
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT I."
     Site            290
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            296
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            302
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            307
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            339
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          401..426
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT I."
     Site            624
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          706..730
```

```
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT II."
     Region          742..765
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT II."
     Region          774..793
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT II."
     Region          800..820
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT II."
     Site            835
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          836..856
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT II."
     Region          910..935
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT II."
     Site            1002
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1019
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1085
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1153..1176
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT III."
     Region          1190..1215
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT III."
     Region          1222..1243
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT III."
     Region          1248..1269
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT III."
     Region          1289..1310
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT III."
     Site            1317
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1331
                     /gene="SCN3A"
```

```
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1393..1419
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT III."
     Region          1473..1496
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT IV."
     Region          1508..1531
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT IV."
     Region          1538..1561
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT IV."
     Region          1572..1593
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT IV."
     Region          1609..1631
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT IV."
     Region          1698..1722
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT IV."
ORIGIN
        1 maqallvppg pesfrlftre slaaiekraa eekakkpkke qdiddenkpk pnsdleagkn
       61 lpfiygdipp emvsepledl dpyyvskktf vvlnkgkaif rfsatsalyi ltplnpvrki
      121 aikilvhslf smlimctilt ncvfmtlsnp pdwtknveyt ftgiytfesl ikilargfcl
      181 edftflrdpw nwldfsvivm ayvtefvdlg nvsalrtfrv lralktisvi pglktivgal
      241 iqsvkklsdv miltvfclsv faliglqlfm gnlrnkcsqw ppsdsafetn ttsyfngtmd
      301 sngtfvnvtm stfnwkdyia ddshfyvldg qkdpllcgng sdagqcpegy icvkagrnpn
      361 ygytsfdtfs waflslfrlm tqdywenlyq ltlraagkty miffvlvifl gsfylvnlil
      421 avvamayeeq nqatleeaeq keaefqqmle qlkkqqeeaq avaaasaasr dfsgigglge
      481 llessseask lssksakewr nrrkkrrqre hlegnhradg drfpksesed svkrrsflls
      541 ldgnpltgdk klcsphqsll sirgslfspr rnsktsifsf rgrakdvgse ndfaddehst
      601 fedsesrrds lfvphrpger rnsngtttet evrkrrlssy qismemleds sgrqrsmsia
      661 siltntmeel eesrqkcppc wyrfanvfli wdccdawlkv khlvnlivmd pfvdlaitic
      721 ivlntlfmam ehypmtqqfs svltvgnlvf tgiftaemvl kiiamdpyyy fqegwnifdg
      781 iivslslmel glanveglsv lrsfrllrvf klakswptln mlikiignsv galgnltlvl
      841 aiivfifavv gmqlfgksyk ecvckinvdc klprwhmndf fhsflivfrv lcgewietmw
      901 dcmevagqtm clivfmlvmv ignlvvlnlf lalllssfss dnlaatdddn emnnlqiavg
      961 rmqkgidfvk nkirecfrka ffrkpkviei qegnkidscm snntgieisk elnylkdgng
     1021 ttsgvgtgss vekyvidend ymsfinnpsl tvtvpiavge sdfenlntee fsseselees
     1081 keklnatsss egstvdvapp regeqaeiep eedlkpeacf tegcikkfpf cqvsteegkg
     1141 kiwwnlrktc ysivehnwfe tfivfmills sgalafediy ieqrktiktm leyadkvfty
     1201 ifilemllkw vaygfqtyft nawcwldfli vdvslvslva nalgyselga ikslrtlral
     1261 rplralsrfe gmrvvvnalv gaipsimnvl lvclifwlif simgvnlfag kfyhcvnttt
     1321 gnmfeikevn nfsdcqalgk qarwknvkvn fdnvgagyla llqvatfkgw mdimyaavds
     1381 rdvklqpiye enlymylyfv ifiifgsfft lnlfigviid nfnqqkkkfg gqdifmteeq
     1441 kkyynamkkl gskkpqkpip rpankfqgmv fdfvtrqvfd isimilicln mvtmmvetdd
     1501 qskymtlvls rinlvfivlf tgefllklis lryyyftigw nifdfvvvil sivgmflael
     1561 iekyfvsptl frvirlarig rilrlikgak girtllfalm mslpalfnig lllflvmfiy
     1621 aifgmsnfay vkkeagiddm fnfetfgnsm iclfqittsa gwdgllapil nsappdcdpd
     1681 aihpgssvkg dcgnpsvgif ffvsyiiisf lvvvnmyiav ilenfsvate esaeplsedd
     1741 femfyevwek fdpdatqfie fcklsdfaaa ldpplliakp nkvqliamdl pmvsgdrihc
     1801 ldilfaftkr vlgesgemda lriqmedrfm asnpskvsye pitttlkrkq eevsaaiiqr
     1861 nyrcyllkqr lknisskydk etikgridlp ikgdmvidkl ngnstpektd gsssttspps
     1921 ydsvtkpdke kfekdkpeke ikgkevrenq k
//
```

Revised: October 24, 2001.

1: P08104. Sodium channel pr...[gi:116449] BLink, Related Sequences, PubMed, Taxonomy, LinkOut

```
LOCUS       CIN3_RAT                1951 aa            linear   ROD 16-OCT-2001
DEFINITION  Sodium channel protein, brain III alpha subunit (Voltage-gated
            sodium channel subtype III).
ACCESSION   P08104
PID         g116449
VERSION     P08104  GI:116449
DBSOURCE    swissprot: locus CIN3_RAT, accession P08104;
            class: standard.
            created: Aug 1, 1988.
            sequence updated: Aug 1, 1988.
            annotation updated: Oct 16, 2001.
            xrefs: gi: 57210, gi: 57211, gi: 92754
            xrefs (non-sequence databases): InterPro IPR002111, InterPro
            IPR000636, InterPro IPR001682, InterPro IPR000048, InterPro
            IPR001696, Pfam PF00520, Pfam PF00612, PRINTS PR00170, SMART
            SM00015
KEYWORDS    Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
            Glycoprotein; Repeat; Multigene family.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (residues 1 to 1951)
  AUTHORS   Kayano,T., Noda,M., Flockerzi,V., Takahashi,H. and Numa,S.
  TITLE     Primary structure of rat brain sodium channel III deduced from the
            cDNA sequence
  JOURNAL   FEBS Lett. 228 (1), 187-194 (1988)
  MEDLINE   88137594
  REMARK    SEQUENCE FROM N.A.
            STRAIN=WISTAR
COMMENT     ---------------------------------------------------------------------
            This SWISS-PROT entry is copyright. It is produced through a
            collaboration between the Swiss Institute of Bioinformatics and
            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
            and http://www.ebi.ac.uk/sprot
            ---------------------------------------------------------------------.
            [FUNCTION] THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT SODIUM ION
            PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
            CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
            MEMBRANE, THE PROTEIN FORMS A SODIUM-SELECTIVE CHANNEL THROUGH
            WHICH NA++ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
            GRADIENT.
            [SUBUNIT] THE SODIUM CHANNEL CONSISTS OF A LARGE POLYPEPTIDE AND
            2-3 SMALLER ONES. THIS SEQUENCE REPRESENTS A LARGE POLYPEPTIDE.
            [SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN.
            [DOMAIN] THE SEQUENCE CONTAINS 4 INTERNAL REPEATS, EACH WITH 5
            HYDROPHOBIC SEGMENTS (S1,S2,S3,S5,S6) AND ONE POSITIVELY CHARGED
            SEGMENT (S4). SEGMENTS S4 ARE PROBABLY THE VOLTAGE-SENSORS AND ARE
            CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
```

```
            EVERY THIRD POSITION.
            [SIMILARITY] TO OTHER SODIUM CHANNEL PROTEINS.
            [SIMILARITY] CONTAINS 1 IQ DOMAIN.
FEATURES             Location/Qualifiers
     source          1..1951
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     gene            1..1951
                     /gene="SCN3A"
     Protein         1..1951
                     /gene="SCN3A"
                     /product="Sodium channel protein, brain III alpha subunit"
     Region          124..147
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT I."
     Region          156..175
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT I."
     Region          189..207
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT I."
     Site            211
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          214..233
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT I."
     Region          249..273
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT I."
     Site            290
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            296
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            302
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            307
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            339
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          401..426
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT I."
     Site            624
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          706..730
```

```
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT II."
     Region          742..765
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT II."
     Region          774..793
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT II."
     Region          800..820
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT II."
     Site            835
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          836..856
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT II."
     Region          910..935
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT II."
     Site            1002
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1019
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1085
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1153..1176
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT III."
     Region          1190..1215
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT III."
     Region          1222..1243
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT III."
     Region          1248..1269
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT III."
     Region          1289..1310
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT III."
     Site            1317
                     /gene="SCN3A"
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Site            1331
                     /gene="SCN3A"
```

```
                     /site_type="glycosylation"
                     /note="N-LINKED (GLCNAC...) (POTENTIAL)."
     Region          1393..1419
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT III."
     Region          1473..1496
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S1 OF REPEAT IV."
     Region          1508..1531
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S2 OF REPEAT IV."
     Region          1538..1561
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S3 OF REPEAT IV."
     Region          1572..1593
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S4 OF REPEAT IV."
     Region          1609..1631
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S5 OF REPEAT IV."
     Region          1698..1722
                     /gene="SCN3A"
                     /region_name="Transmembrane region"
                     /note="S6 OF REPEAT IV."
ORIGIN
        1 maqallvppg pesfrlftre slaaiekraa eekakkpkke qdiddenkpk pnsdleagkn
       61 lpfiygdipp emvsepledl dpyyvskktf vvlnkgkaif rfsatsalyi ltplnpvrki
      121 aikilvhslf smlimctilt ncvfmtlsnp pdwtknveyt ftgiytfesl ikilargfcl
      181 edftflrdpw nwldfsvivm ayvtefvdlg nvsalrtfrv lralktisvi pglktivgal
      241 iqsvkklsdv miltvfclsv faliglqlfm gnlrnkcsqw ppsdsafetn ttsyfngtmd
      301 sngtfvnvtm stfnwkdyia ddshfyvldg qkdpllcgng sdagqcpegy icvkagrnpn
      361 ygytsfdtfs waflslfrlm tqdywenlyq ltlraagkty miffvlvifl gsfylvnlil
      421 avvamayeeq nqatleeaeq keaefqqmle qlkkqqeeaq avaaasaasr dfsgigglge
      481 llessseask lssksakewr nrrkkrrqre hlegnhradg drfpksesed svkrrsflls
      541 ldgnpltgdk klcsphqsll sirgslfspr rnsktsifsf rgrakdvgse ndfaddehst
      601 fedsesrrds lfvphrpger rnsngtttet evrkrrlssy qismemleds sgrqrsmsia
      661 siltntmeel eesrqkcppc wyrfanvfli wdccdawlkv khlvnlivmd pfvdlaitic
      721 ivlntlfmam ehypmtqqfs svltvgnlvf tgiftaemvl kiiamdpyyy fqegwnifdg
      781 iivslslmel glanveglsv lrsfrllrvf klakswptln mlikiignsv galgnltlvl
      841 aiivfifavv gmqlfgksyk ecvckinvdc klprwhmndf fhsflivfrv lcgewietmw
      901 dcmevagqtm clivfmlvmv ignlvvlnlf lalllssfss dnlaatdddn emnnlqiavg
      961 rmqkgidfvk nkirecfrka ffrkpkviei qegnkidscm snntgieisk elnylkdgng
     1021 ttsgvgtgss vekyvidend ymsfinnpsl tvtvpiavge sdfenlntee fsseselees
     1081 keklnatsss egstvdvapp regeqaeiep eedlkpeacf tegcikkfpf cqvsteegkg
     1141 kiwwnlrktc ysivehnwfe tfivfmills sgalafediy ieqrktiktm leyadkvfty
     1201 ifilemllkw vaygfqtyft nawcwldfli vdvslvslva nalgyselga ikslrtlral
     1261 rplralsrfe gmrvvvnalv gaipsimnvl lvclifwlif simgvnlfag kfyhcvnttt
     1321 gnmfeikevn nfsdcqalgk qarwknvkvn fdnvgagyla llqvatfkgw mdimyaavds
     1381 rdvklqpiye enlymylyfv ifiifgsfft lnlfigviid nfnqqkkkfg gqdifmteeq
     1441 kkyynamkkl gskkpqkpip rpankfqgmv fdfvtrqvfd isimilicln mvtmmvetdd
     1501 qskymtlvls rinlvfivlf tgefllklis lryyyftigw nifdfvvvil sivgmflael
     1561 iekyfvsptl frvirlarig rilrlikgak girtllfalm mslpalfnig lllflvmfiy
     1621 aifgmsnfay vkkeagiddm fnfetfgnsm iclfqittsa gwdgllapil nsappdcdpd
     1681 aihpgssvkg dcgnpsvgif ffvsyiiisf lvvvnmyiav ilenfsvate esaeplsedd
     1741 femfyevwek fdpdatqfie fcklsdfaaa ldpplliakp nkvqliamdl pmvsgdrihc
     1801 ldilfaftkr vlgesgemda lriqmedrfm asnpskvsye pitttlkrkq eevsaaiiqr
     1861 nyrcyllkqr lknisskydk etikgridlp ikgdmvidkl ngnstpektd gsssttspps
     1921 ydsvtkpdke kfekdkpeke ikgkevrenq k
//
```

Revised: October 24, 2001.